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OM nucleic - nucleic search, using sw model

Run on: April 30, 2006, 10:42:19 ; Search time 949 Seconds  
(without alignments)  
10195.124 Million cell updates/sec

Title: US-10-626-398-7  
Perfect score: 1170  
Sequence: 1 atgttggaataaacagtagc.....accgtcaatataccacttga 1170

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA\_Main:\*  
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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	1170	8	US-10-626-445-7
2	1170	100.0	1170	9	US-10-626-126-7
3	1170	100.0	1170	9	US-10-626-398-7
4	675	57.7	1170	9	US-10-488-421-7
5	675	57.7	1173	3	US-09-812-216-1
6	675	57.7	1173	3	US-09-910-411-1
7	675	57.7	1173	3	US-09-875-076-13
8	675	57.7	1173	3	US-09-876-252-13
9	675	57.7	1173	5	US-10-052-193-1
10	675	57.7	1173	6	US-10-272-983-13
11	675	57.7	1173	6	US-10-354-769-1
12	675	57.7	1173	6	US-10-393-807-13
13	675	57.7	1173	6	US-10-417-820A-13
14	675	57.7	1173	7	US-10-349-253A-1
15	675	57.7	1173	7	US-10-723-955-13
16	675	57.7	1173	7	US-10-782-596-13
17	675	57.7	1173	7	US-10-737-619-1
18	675	57.7	1173	8	US-10-626-445-1
19	675	57.7	1173	9	US-10-616-088-1
20	675	57.7	1173	9	US-10-626-126-1
21	675	57.7	1173	9	US-10-626-398-1
22	675	57.7	1173	9	US-10-723-955-13
23	675	57.7	1266	3	US-09-891-138A-5

## ALIGNMENTS

RESULT 1  
US-10-626-445-7  
; Sequence 7, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626, 445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790, 849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208, 260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
US-10-626-445-7

Query Match	Best Local Similarity	Score	DB 8;	Length	1170;
Matches	1170;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
Qy	1	ATGTTGGCAATTAACAGTCAATCGGCTTAACATCAATTAATAATTTCTTTGACATTTTAA	60		
Db	1	ATGTTGGCAATTAACAGTCAATCGGCTTAACATCAATTAATAATTTCTTTGACATTTTAA	60		
Qy	61	ATGCTTTTACTAGCTATTCCTAATGTTAGGCAATGCTGCTGCTCATTTTATTTAGCTTTTAT	120		
Db	61	ATGCTTTTACTAGCTATTCCTAATGTTAGGCAATGCTGCTGCTCATTTTATTTAGCTTTTAT	120		
Qy	121	GTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACCTTGGCCATTTGCAGAC	180		
Db	121	GTGGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACCTTGGCCATTTGCAGAC	180		
Qy	181	TTCTTTTGGGTGCAATTCCTCTGTATCATCATCTTCCTCGCTGACTTACTGACT	240		
Db	181	TTCTTTTGGGTGCAATTCCTCTGTATCATCATCTTCCTCGCTGACTTACTGACT	240		
Qy	241	TCCTGGAAAGCAAGCTTGTGTTATTTTGGCTCATTTACTGACTATCTTTTATGACAGCATCT	300		
Db	241	TCCTGGAAAGCAAGCTTGTGTTATTTTGGCTCATTTACTGACTATCTTTTATGACAGCATCT	300		

301 GTGTATAATATTGTCCTCATCAGTCAGTACGATCGCTACCAATGCGTGTGG 360  
Db GTGTATAATATTGTCCTCATCAGTCAGTACGATCGCTACCAATGCGTGTGG 360  
361 TATAGAGCTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
Db TATAGAGCTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
421 TTCTCTTCAATGCAATATGGCGCGATGATTTCTGATTTTCAGACTCTTGGCAGAAATAGCACT 480  
Db TTCTCTTCAATGCAATATGGCGCGATGATTTCTGATTTTCAGACTCTTGGCAGAAATAGCACT 480  
481 ACAGAAATGCAACTGGAATTTTAAATAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db ACAGAAATGCAACTGGAATTTTAAATAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
541 GAATTCCTGTATCCCATCTTTGTTAGTTGCTTAATTCAGCGCCCATATTTTACTGGAGCCTG 600  
Db GAATTCCTGTATCCCATCTTTGTTAGTTGCTTAATTCAGCGCCCATATTTTACTGGAGCCTG 600  
601 TGAAGCGAGAGAAACTGAGCAGGTGCTCAGCCACCGCTGTACTCCCTCTGACTCTCTCTCC 660  
Db TGAAGCGAGAGAAACTGAGCAGGTGCTCAGCCACCGCTGTACTCCCTCTGACTCTCTCTCC 660  
661 AGCAGTGAACCAAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGACTCTGCCAGCA 720  
Db AGCAGTGAACCAAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGACTCTGCCAGCA 720  
721 CGAAAGAAACAACTGCTCTCTCTGTTTCAGACAAGTCAAGGAGAGAGCACTCTCTTTG 780  
Db CGAAAGAAACAACTGCTCTCTCTGTTTCAGACAAGTCAAGGAGAGAGCACTCTCTTTG 780  
781 TTTTCCATAGAGCCTCAAGAAACAGCAATGTGATCGCTTCCAAAATGGGCTTCTCTCTCC 840  
Db TTTTCCATAGAGCCTCAAGAAACAGCAATGTGATCGCTTCCAAAATGGGCTTCTCTCTCC 840  
841 CACTCAGATTCCTGGCTCTTACGAAAGGAAACATATCGACTTTTTCAGAGCAGGAAA 900  
Db CACTCAGATTCCTGGCTCTTACGAAAGGAAACATATCGACTTTTTCAGAGCAGGAAA 900  
901 TTAGCCAAAGTCACTGGCCATCTTTAGCAGCTTTTGGCAATTTGCTGGCTCCATATTC 960  
Db TTAGCCAAAGTCACTGGCCATCTTTAGCAGCTTTTGGCAATTTGCTGGCTCCATATTC 960  
961 CTGACTACAGTTATCTACTCAATTTTCTCTGAAAGGAACTTGACTAAATCAACTGGTAC 1020  
Db CTGACTACAGTTATCTACTCAATTTTCTCTGAAAGGAACTTGACTAAATCAACTGGTAC 1020  
1021 CATACTGCTTTTGGCTCCAGTGTTCATTTCTTTGTTAATCCCTTTTGTATCCATTG 1080  
Db CATACTGCTTTTGGCTCCAGTGTTCATTTCTTTGTTAATCCCTTTTGTATCCATTG 1080  
1081 TGTCAAAAGCTTTTTCAGAGGCTTTCTGAAATATCTTCTCTGAGAGGCAATCCACG 1140  
Db TGTCAAAAGCTTTTTCAGAGGCTTTCTGAAATATCTTCTCTGAGAGGCAATCCACG 1140  
1141 CCACCAACAAACCGCTCAATATCCACTTGA 1170  
Db CCACCAACAAACCGCTCAATATCCACTTGA 1170

RESULT 2  
US-10-626-126-7  
; Sequence 7, Application US/10626126  
; Publication No. US20050074770A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCES: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
; US-10-626-126-7  
  
Query Match 100.0%; Score 1170; DB 9; Length 1170;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGTTGGCAAAATTAACAGTACAAATCGCTTTAAACATCAATCAATTTTAAATTTCTTTGACATTTTAA 60  
Db 1 ATGTTGGCAAAATTAACAGTACAAATCGCTTTAAACATCAATCAATTTTAAATTTCTTTGACATTTTAA 60  
61 ATGTCCTTTACTAGCTAATGCTATAATGTTAGGCAATGTCGTGCTCAATTTTAGCTTTTATT 120  
Db 61 ATGTCCTTTACTAGCTAATGCTATAATGTTAGGCAATGTCGTGCTCAATTTTAGCTTTTATT 120  
121 GTGGACAGAAATCTTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTGCAGAC 180  
Db 121 GTGGACAGAAATCTTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTGCAGAC 180  
181 TTCTTTTGGGTGCAATGCAATTCCTCTGTACATACCTTCTCGCTGACTTTACTGGACT 240  
Db 181 TTCTTTTGGGTGCAATGCAATTCCTCTGTACATACCTTCTCGCTGACTTTACTGGACT 240  
241 TCTGGAAAGCAAGCTTGTGTATTTTGGCTCAATTAATTTTATTTATGTACAGCATCT 300  
Db 241 TCTGGAAAGCAAGCTTGTGTATTTTGGCTCAATTAATTTTATTTATGTACAGCATCT 300  
301 GTGTATAATATTGTCCTCATCAGTACGATCGCTACAGTACGATCGCTACAGTCTCAAAATGCGTGTGG 360  
Db 301 GTGTATAATATTGTCCTCATCAGTACGATCGCTACAGTACGATCGCTACAGTCTCAAAATGCGTGTGG 360  
361 TATAGAGCTCAGCACTCTGGCACCTGGAAAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
Db 361 TATAGAGCTCAGCACTCTGGCACCTGGAAAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420  
421 TTCTCTCTCATCAGAAATGCGCGATGATTTCTGATTTTCAGACTCTTTGGCAGAAATAGCACT 480  
Db 421 TTCTCTCTCATGACAAATGGCGGATGATTTCTGATTTTCAGACTCTTTGGCAGAAATAGCACT 480  
481 ACAGAAATGCAACTGGAATTTTAAATAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db 481 ACAGAAATGCAACTGGAATTTTAAATAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
541 GAATTCCTGTATCCCATCTTTGTTAGTTGCTTAATTCAGCGCCCATATTTTACTGGAGCCTG 600  
Db 541 GAATTCCTGTATCCCATCTTTGTTAGTTGCTTAATTCAGCGCCCATATTTTACTGGAGCCTG 600  
601 TGAAGCGAGAGAAACTGAGCAGGTGCTCAGCCACCGCTGTACTCCCTCTGACTCTCTCTCC 660  
Db 601 TGAAGCGAGAGAAACTGAGCAGGTGCTCAGCCACCGCTGTACTCCCTCTGACTCTCTCTCC 660  
661 AGCAGTGAACCAAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGACTCTGCCAGCA 720  
Db 661 AGCAGTGAACCAAGCACTCTCTGAGCAGGACCCGATTTCAAGGCGGACTCTGCCAGCA 720  
721 CGAAAGAAACAACTGCTCTCTCTGTTTCAGACAAGTCAAGGAGAGAGCACTCTCTTTG 780  
Db 721 CGAAAGAAACAACTGCTCTCTCTGTTTCAGACAAGTCAAGGAGAGAGCACTCTCTTTG 780  
781 TTTTCCATAGAGCCTCAAGAAACAGCAATGTGATCGCTTCCAAAATGGGCTTCTCTCTCC 840  
Db 781 TTTTCCATAGAGCCTCAAGAAACAGCAATGTGATCGCTTCCAAAATGGGCTTCTCTCTCC 840  
841 CACTCAGATTCCTGGCTCTTACGAAAGGAAACATATCGACTTTTTCAGAGCAGGAAA 900

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Db      |||||
841     CACTCAGATTCCCTGGCTCTTCAGCAAGGAGACATATCGAACTTTTCAGAGCCAGGAAA 900
Qy      |||||
901     TTAGCAAGTCACTGGCCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTCA 960
Db      |||||
901     TTAGCAAGTCACTGGCCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTCA 960
Qy      |||||
961     CTGACTACAGTTATCTACTCAATTTTCTCGAAGGAACTTGACTAAATCAACCTGGTAC 1020
Db      |||||
961     CTGACTACAGTTATCTACTCAATTTTCTCGAAGGAACTTGACTAAATCAACCTGGTAC 1020
Qy      |||||
1021    CATATGCTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCCATTTG 1080
Db      |||||
1021    CATATGCTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCCATTTG 1080
Qy      |||||
1081    TGTCAAAACGTTTTCAGAGGCTTTCCTGAAAATACATCTCTGTGAGAGGAATCCACG 1140
Db      |||||
1081    TGTCAAAACGTTTTCAGAGGCTTTCCTGAAAATACATCTCTGTGAGAGGAATCCACG 1140
Qy      |||||
1141    CCACCACAACCGCTCAATATCCACTTGA 1170
Db      |||||
1141    CCACCACAACCGCTCAATATCCACTTGA 1170
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## RESULT 3

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US-10-626-398-7
; Sequence 7, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Liou, Changlu
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-398-7
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Query Match      100.0%; Score 1170; DB 9; Length 1170;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTTGGCAATAACAGTACAAATCGCCTTAAACATCAATTAATAATTTCTTTGACATTTTAA 60
Db      1 ATGTTGGCAATAACAGTACAAATCGCCTTAAACATCAATTAATAATTTCTTTGACATTTTAA 60
Qy      61 ATGTCCTTTACTAGCTATGCTATTAATGTAGGCAATGTCTGGGTCATTTAGCTTTTATT 120
Db      61 ATGTCCTTTACTAGCTATGCTATTAATGTAGGCAATGTCTGGGTCATTTAGCTTTTATT 120
Qy      121 GTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTTGGCCATTCGACAG 180
Db      121 GTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTTGGCCATTCGACAG 180
Qy      181 TTCTTTTGGGTGCAATTGCAATTTCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240
Db      181 TTCTTTTGGGTGCAATTGCAATTTCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240
Qy      241 TCTGGAAGCAAGCTTGTTATTTTGGTCAATTAATGCTATCTTTTATGTAAGCAATCT 300
Db      241 TCTGGAAGCAAGCTTGTTATTTTGGTCAATTAATGCTATCTTTTATGTAAGCAATCT 300
Qy      301 GTGTATATATTTGCTTCATCAGTACGATCGCTACCAAGTCAAGTCTCAATGCGGTGG 360
Db      |||||
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## RESULT 4

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US-10-488-421-7
; Sequence 7, Application US/10488421
; Publication No. US20050239065A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc. [US/US]
; APPLICANT: Gallagher, Michael J.
; APPLICANT: Yates, Stephen L.
; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES
; FILE REFERENCE: 1367-13335WO01
; CURRENT APPLICATION NUMBER: US/10/488,421
; CURRENT FILING DATE: 2004-03-01
; PRIOR APPLICATION NUMBER: US 60/316,762
; PRIOR FILING DATE: 2001-08-31
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Db      |||||
301     GTGTATAATATTGTCCTCATCAGCTACGATCGCTACCACTCAGTCTCAAAATGCGCGTGTGG 360
Qy      |||||
361     TATAGAGCTCAGCACTCTGGCACTCTGGCAAAATTTGCTACTCAGATGGTGGCTGTGTTGGATA 420
Db      |||||
361     TATAGAGCTCAGCACTCTGGCACTCTGGCAAAATTTGCTACTCAGATGGTGGCTGTGTTGGATA 420
Qy      |||||
421     TTCTCCTTCATGACAAATGGGCCGATGATCTTGATTTTCAGACTCTTTGGCAGAAATAGCACT 480
Db      |||||
421     TTCTCCTTCATGACAAATGGGCCGATGATCTTGATTTTCAGACTCTTTGGCAGAAATAGCACT 480
Qy      |||||
481     ACAGAAATGTGAACCTGGATTTTAAAAAAGTGTACTTTTGCTCTCCCTACATCATATTATG 540
Db      |||||
481     ACAGAAATGTGAACCTGGATTTTAAAAAAGTGTACTTTTGCTCTCCCTACATCATATTATG 540
Qy      |||||
541     GAATTCCTGATCCCGATCTTGTAGTTGCTTATTTTCAGCGGCCCATATTATTCAGAGCCCTG 600
Db      |||||
541     GAATTCCTGATCCCGATCTTGTAGTTGCTTATTTTCAGCGGCCCATATTATTCAGAGCCCTG 600
Qy      |||||
601     TGGAAAGCGAGAGAACTGAGCAGGTGCTCAGCCACCCCTGTACTCCCTCTGACTCTTCTCC 660
Db      |||||
601     TGGAAAGCGAGAGAACTGAGCAGGTGCTCAGCCACCCCTGTACTCCCTCTGACTCTTCTCC 660
Qy      |||||
661     AGCAGTGACCAACGAGCACTCTCTGACAGCAGGACCCCGATTTCAGGGCGACTCTTGCAGCA 720
Db      |||||
661     AGCAGTGACCAACGAGCACTCTCTGACAGCAGGACCCCGATTTCAGGGCGACTCTTGCAGCA 720
Qy      |||||
721     CGGAAAGAAACAATCGCTCTCTTGGTTTCAGCAAGTCAACGAGAGAAAGAGCAGTCTCTTTG 780
Db      |||||
721     CGGAAAGAAACAATCGCTCTCTTGGTTTCAGCAAGTCAACGAGAGAAAGAGCAGTCTCTTTG 780
Qy      |||||
781     TTTTCCATAGAGAGCTACAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840
Db      |||||
781     TTTTCCATAGAGAGCTACAGAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCTCC 840
Qy      |||||
841     CACTCAGATTCCTCGGCTCTTTCAGCAAGGAAACATATCGAACTTTTCAGAGCCAGGAAA 900
Db      |||||
841     CACTCAGATTCCTCGGCTCTTTCAGCAAGGAAACATATCGAACTTTTCAGAGCCAGGAAA 900
Qy      |||||
901     TTAGCAAGTCACTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTCA 960
Db      |||||
901     TTAGCAAGTCACTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTCA 960
Qy      |||||
961     CTGACTACAGTTATCTACTCAATTTTCTCGAAGGAACTTGACTAAATCAACCTGGTAC 1020
Db      |||||
961     CTGACTACAGTTATCTACTCAATTTTCTCGAAGGAACTTGACTAAATCAACCTGGTAC 1020
Qy      |||||
1021    CATATGCTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCCATTTG 1080
Db      |||||
1021    CATATGCTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCCATTTG 1080
Qy      |||||
1081    TGTCAAAACGTTTTCAGAGGCTTTTCTGAAAATACCTTCTGTGAGAGGAATCCACG 1140
Db      |||||
1081    TGTCAAAACGTTTTCAGAGGCTTTTCTGAAAATACCTTCTGTGAGAGGAATCCACG 1140
Qy      |||||
1141    CCACCACAACCGCTCAATATCCACTTGA 1170
Db      |||||
1141    CCACCACAACCGCTCAATATCCACTTGA 1170
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; PRIOR APPLICATION NUMBER: US 60/332,697  
 ; PRIOR FILING DATE: 2001-11-13  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1170  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1170)  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent  
 ; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.  
 ; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence  
 ; OTHER INFORMATION: only  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462  
 ; OTHER INFORMATION: are AAG and 988 is C  
 ; US-10-488-421-7

Query Match 57.7%; Score 675; DB 9; Length 1170;  
 Best Local Similarity 74.9%; Pred. No. 7.5e-185;  
 Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy	8	CAAAATACAGTACATCGCCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGCTTT	67
Db	11	CTAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTTTTTATGTCCT	70
Qy	68	TACTAGCTATTGCTATATAAGTCTAGGCAATCGTCGTGTCATTTTATGTCGACA	127
Db	71	TAGTAGCTTTTGCTATATGCTAGAAATGCTTTGGTCATTTAGCTTTTGTGTGACACA	130
Qy	128	GAATCTTAGACATCGAAGTAAATTAATTTTCTTAACTTGGCCATTCGACAGCTTCTTTG	187
Db	131	AAAACCTTAGACATGGAAGTAGTTATTTTTTCTTAACTTGGCCATCTCTGACTTCTTTG	190
Qy	188	TGGGTGCAATTGCAATTCCTCTGTACATACCTTCCTCGCTGACTTACTGAGCTTCGGAA	247
Db	191	TGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTTCTGAATGGAATTTTGGAA	250
Qy	248	AGCAAGCTTCGTATTTTGGCTCATTTACTGACTATCTTTTATGTCAGCAATCTGTGTATA	307
Db	251	AGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCAATCTGTATATA	310
Qy	308	ATATTGTCCTCATCAGCTACGATCGCTACAGTCAGTCTCAAAATGCCGTGTGTTATAGAG	367
Db	311	ACATTGTCCTCATCAGCTATATGATGATACCTGTGTCAGTCTCAAAATGCTGTCTTATAGAA	370
Qy	368	CTCAGCACTCTGGCACTCGGAAATGCTACTCAGATGFTGGCTGTTTGGATATTTCTCCT	427
Db	371	CTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGATGTTGGCGGTTTGGGTGCTGGCCT	430
Qy	428	TCTATGCAAAATGGCCGATCATTTCTGATTTTTCAGACTCTTTGGCAGNATAGCACTACAGAT	487
Db	431	TCATTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAGGATGAAAGGTAGTGAAT	490
Qy	488	GTGAACCTGGATTTTTTAAAAAAGTGTACTTTTGTCTCTCCCTACATCATTTATTCGAATTC	547



Query Match 57.7%; Score 675; DB 3; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 7.5e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCGCCTTAACATCAATTAATAAATCTTTGACATTTTAAATGTCTT 67  
Db 11 CTAATAGACCAATCAATTTATACATTAAGCACTCGTGTACTTTAGCAATTTTATGTCTT 70

Qy 68 TACTAGCTATTGCTATTAATGTTAGCAATGCGGTGCTCAATTTAGCTTTTATGTGGACA 127  
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Qy 128 GAATCTTTAGACATCGAATTAATTAATTTTCTTAACCTTGCCATTCGACATTCCTTTG 187  
Db 131 AAAACCTTTAGACATCGAATTAATTTTCTTAACCTTGCCATTCGACATTCCTTTG 190

Qy 188 TGGGTGCAATTTGCAATTCCTCTGTACATACCTCTCGCTGACTTACTTGGACTTCTGAA 247  
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Db 431 TCTTAGTGAATGGGCGCAATGATTCGATTTTCTGAGTCTTTGGAAGATGAAGTAGTGAAT 490

Qy 488 GTGAACCTGGATTTTAAAGTGGTACTTTGCTCTCCCTACATCAATTAATGGAATTC 547  
Db 491 GTGAACCTGGATTTTAAAGTGGTACTTTGCTCTCCCTACATCAATTAATGGAATTC 550

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Qy 968 CAGTTACTACTCATTTTCTTCTGAAAGAACTTTGACTTAATCAACCTGGTACCATCTG 1027  
Db 968 CAATTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1027

## RESULT 6

US-09-910-411-1  
; Sequence 1, Application US/09910411  
; Patent No. US20020137054A1  
; GENERAL INFORMATION:  
; APPLICANT: Bergema, Derek  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Li, Xiatong  
; APPLICANT: Michalovich, David  
; APPLICANT: Zhu, Yuan  
; TITLE OF INVENTION: AKOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GP70655-2C1  
; CURRENT APPLICATION NUMBER: US/09/910,411  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-910-411-1

Query Match 57.7%; Score 675; DB 3; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 7.5e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCGCCTTAACATCAATTAATAAATCTTTGACATTTTAAATGTCTT 67  
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Qy 1148 ACACCG 1154
Db 1148 AACACAG 1154
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US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
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Query Match 57.7%; Score 675; DB 3; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACAAATCGCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTTTATGTCCT 70
Qy 68 TACTAGCTATGCTATTAATGTTAGGCAATGCTGGTCAATTTAGCTTTTATGTCGACA 127
Db 71 TAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGGTCAATTTTGTGTCGACA 130
Qy 128 GAAATCTTACACATCGAAGTAAATTTACTTTTCTTAATCTTGGCCATTCGACACTTTTG 187
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Qy 368 CTCAGCACTCTGGCACTGGAATGCTACTCAGATGGTGGCTGTTTGGATATTTCTCT 427
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Db 1148 AACACAG 1154

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US-09-876-252-13  
; Sequence 13, Application US/09876252  
; Publication No. US20030018182A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Re  
; FILE REFERENCE: ARN-0054  
; CURRENT APPLICATION NUMBER: US/09/876,252  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
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; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,946  
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; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/152,524  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/151,114  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/108,029  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
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; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
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; PRIOR APPLICATION NUMBER: 60/157,281  
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; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-876-252-13

Query Match 57.7%; Score 675; DB 3; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 7.5e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
QY 8 CAATACAGTACATCGCTTACATCAATTAATAATTTCTTTCACATTTTATATGCTT 67  
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Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCAATTTTTATGTCTT 70
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; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1
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Query Match 57.7%; Score 675; DB 5; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
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Db 11 CTAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCAATTTTATGTCTT 70
Qy 68 TACTAGCTATTGCTATTAATGTTAGGCAATGTCGTGTCAATTTAGCTTTTATGTCGACA 127
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Db 551 TGATCCCCATCTTGTAGTCTTATTTTCAACATGAATATTTTATGGAGCTGTGGAGC 610
Qy 608 GAGAGAACTGAGCAGGCTTCCAGCCACCTGCTGCTCTCCCTGCTGCTCTTCCAGCAGTG 667
Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTGAGCTGACTGCTCTCTTCCAAACA --- 667
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Db 908 AGTCACCTGGCCATCTCTTAGGGGTTTTGCTGTTTGTCTGGGCTCCATATCTCTGTTC 967  
Qy 968 CAGTTATCTACTCAATTTTTCTGAAAGAACTTGACATAAATCAACCTGGTACCATCTG 1027  
Db 968 CAATGTCTCTTCAATTTATTTCTCTCAGCAAGAGTCCATAATCAAGTTGGTATAGAAATG 1027  
Qy 1028 CTTTTGGCTCCAGTGGTTCAATTTCTTTGTTAATCCCTTTTTGTATCCATTTGTGTGAC 1087  
Db 1028 CATTTGGCTTCAAGTGGTTCAATTTCTTTGTCATCTCTTTGTATCCATTTGTATGTCACA 1087  
Qy 1088 AACGTTTTCAAGAGCTTTCTGAAAAATACCTCTGTGAGAGGAATCCACGCCACAC 1147  
Db 1088 AGCGTTTTCAAGAGCTTTCTTTGAAAAATATTTGTATAAAAAAGCAACCTCTACCATCAC 1147  
Qy 1148 ACAACCG 1154  
Db 1148 AACACAG 1154

RESULT 11  
US-10-354-769-1  
; Sequence 1, Application US/10354769  
; Publication No. US20030149242A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: O'Reilly, Mark A.  
; APPLICANT: Peter Beate  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
; FILE REFERENCE: PCI0373B  
; CURRENT APPLICATION NUMBER: US/10/354,769  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 09/698,801  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/211,243  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: GB 9925641.4  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: GB 0009973.9  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-354-769-1

Query Match 57.7%; Score 675; DB 6; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 7.5e-185;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAATATACGTACCAATCCGCTTAACATCAATATAAATTTCTTGACATTTTAAATGTCTT 67  
Db 11 CTAATAGCACCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTTTATGTCTT 70  
Qy 68 TACTAGCTATTGCTATATATGTAGCAATGCGGTCAATTTAGCTTTTATGTGGACA 127  
Db 71 TAGTAGCTTTTGCTATAATGCTAGGAATGCTTTGGTCAATTTTACCTTTTGTGGTGGACA 130  
Qy 128 GAAATCTTACAGATCAAGTAAATTAATTTTCTTAACCTTGGCCATTTGACAGATCTTTTG 187  
Db 131 AAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCTGACTTCTTTG 190  
Qy 188 TGGGTGCAATGGCAATCTCTCTGTACATACCTTCTCGCTGACTTACTGGACTTCTGGAA 247  
Db 191 TGGGTGTGATCTCCATCTCTTTGTATACATCCCTCCACAGCTGTTCGAATGGGAATTTGGAA 250  
Qy 248 AGCAAGCTTTGTATTTTGGCTTCAATTAAGTACTATCTTTTATGTACAGATCTGTGTATA 307  
Db 251 AGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCATCTGTATATA 310  
Qy 308 ATATTGCTCTCATCAGCTACGATCGTACACAGTCTCAAAATGCCGTGGGTATAGAG 367

Db 311 ACATTTGCTCTACAGCTATGATCGATACCTGTCACTCTCAAAATGCTGTCTCTTATAGAA 370  
Qy 368 CTGAGCACTCTGCGCACCTGGAATAATGCTACTACTCAGATGGTGGCTGTGTGTGATATTTCTCCT 427  
Db 371 CTCAACATACTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCCGTTTGGGTGCTGGCCT 430  
Qy 428 TCATGACAAATGGGCCGAGTATCTGATTTTTCAGACTCTTGTGGCAGAAATAGCACTACAGAA 487  
Db 431 TCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGGATGAAGGTAGTGAAT 490  
Qy 488 GTGAACCTCGAATTTTAAAAAAGTGGTACTTTGCTCTCCCTACATCATATTTGGAATTC 547  
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Qy 608 GAGAGAACTGAGCAGGTCTCTCAGCCACCTCTGTACTCCCTCTGACTCTTTCACGAGTG 667  
Db 611 GTGATCATCTCAGTAGTGCCAAAGCCATCTCTGAGCTGACTGTCTCTCTTCCAACA --- 667  
Qy 668 ACCAGGACACTCTCTGACAGACAGACCCCGATTTCAAGGGCGACTCTGCCAGCAGGAAAG 727  
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Db 788 CAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTCTCTTCCCAATCAG 847  
Qy 848 ATTCCCTGGCTCTTTCAGAAAGGAAATATCGAATCTTTTTCAGAGCCAGGAATTAGCCA 907  
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Db 908 AGTCACCTGGCCATCTCTTAGGGGTTTGTGCTGTTGCTGGGCTCCATATTTCTCTGTTCA 967  
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Db 968 CAATTTGCTCTTCAATTTATTCCTCAGCAACAGGTCTCTAAATCAGTTTGGTATAGAAATG 1027  
Qy 1028 CTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCATTTGTGTGTCACA 1087  
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Qy 1088 AACGTTTTTCAGAGGGCTTTCTCTGAAATACTTCTCTGTGAGAAAGCAATCCACGCCACAC 1147  
Db 1088 AGCGTTTTCAAAGGCTTTCTTGAAATATTTTGTATAAAAAAGCAACCTCTACCATCAC 1147  
Qy 1148 ACAACCG 1154  
Db 1148 AACACAG 1154

RESULT 12  
US-10-393-807-13  
; Sequence 13, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044



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; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-393-807-13

Query Match      57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7,5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATAACAGTACCAATCCGCTTAACATCAATATAAAATTTCTTGGACATTTTAAATGCTT 67
Db 11 CTAATAGCACAATCAATTTATCACTAAGCACTCGGTGTACTTTAGCATTTTATGTCCT 70

Qy 68 TACTAGCTATTGCTATATGTTAGGCATGTCGGTCAATTTAGCTTTTATTTGGACA 127
Db 71 TAGTAGCTTTTGGCTATATAGCTAGGAATGCTTTGGTCAATTTAGCTTTTGGTGGACA 130

Qy 128 GAAATCTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTCAGACTTCTTTG 187
Db 131 ABAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATTCAGACTTCTTTG 190

Qy 188 TGGGTGCAATGCAATTCCTGTACATACCTTCTCGCTGACTTACTGTGACTTCTGGAA 247
Db 191 TGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGGGATTTGGAA 250

Qy 248 AGCAAGCTTGTGATTTTGGCTCATTAAGTACTATCTTTTATGTACAGCATCTGTGTATA 307
Db 251 AGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCATCTGTATATA 310

Qy 308 ATATTGCTCTCATAGCTACGATCGCTACAGTCACTCAAAATGCGGTGGTATAGAG 367
Db 311 ACATTGCTCTCATAGCTATGATGATACCTGTGAGTCTCAATGCTGTGCTTATAGAA 370

Qy 368 CTCAGCACTCTGGCACTGGAAAAATGCTACTCAGATGGTGGCTGTTTGGATATTTCTCCT 427
Db 371 CTCAACATCTGGGCTCTTGAAGATTGTACTCTGATGTGGCTGTTTGGGTGCTGGCT 430

Qy 428 TCATGACAAATGGGCGGATGATTCGATTTAGACTCTTGGCAGAAATAGCACTACAGAT 487
Db 431 TCTTAGTGAATGGGCGCAATGATTTCTAGTTTTCAGAGTCTTGGAGGATGAAGTAGTAAT 490

Qy 488 GTGAACCTGGAATTTTAAAGTGGTACTTTGCTCTCCCTACATCAATTTGGAATTC 547
Db 491 GTGAACCTGGAATTTTTCGGAATGGTATACCTCTTGGCATCACATCATTTTGAATTCG 550

Qy 548 TGAATCCCATCTTGTAGTGTCTTATTTTTCAGGCGCCATATTTTACTTGGAGCCTGTGGAGC 607
Db 551 TGAATCCCATCTTGTAGTGTCTTATTTTCAACATGATATTTTATTTGGAGCCTGTGGAGC 610

Qy 608 GAGAGAACTGAGCAGGTGGCTTCAGCCACCTCTGACTCTCCCTCTGACTCTTCCAGCAGTG 667
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Db 611 GTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGCACTGACTGCTGTCTCTTCCACA --- 667
Qy 668 ACCACGGACACTCTCTGCAGACAGGACCCCGAATCAAGGGCGACTCTGCGCAGCAGGAAAG 727
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Qy 728 AAACAACGTGCTCTCTTGGTTCAGACCAAGTCAACGGAGAAAGAGAGTCTCTTGTGTTTCCA 787
Db 728 AAGTTCTGCAATCTTTCATTTTCAGAGAGACAGAGGAGAAAGAGTAGTCTCAATGTTTTTCT 787
Qy 788 TAAGAGGCTTCAAGAAACAGCAATCTGATCGCTTCCAAAATGGGCTTCTCTCCCACTCAG 847
Db 788 CAAGAACCAAGATGATAGCAATTCATTTGCTTCCAAAATGGGTTCTTCTCCCACTCAG 847
Qy 848 ATTCCTGCTCTTTCAGCAAGGGAACATATCGAACTTTTCAGAGCCAGGAAATTAGCCA 907
Db 848 ATTCGTAGCTCTTTCAGCAAGGGAACATATGTAACCTGCTTAGAGCCAGGAGATTAGCCA 907
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Qy 968 CAGTTATCTACTCATTTTCTGAAAGGAACCTTGACTTAAATCAACCTGGTACCATACTG 1027
Db 968 CAATTGCTCTTTCATTTTATTCCTCAGCAACAGGCTCTAAATCAAGTTGGTATAGATTG 1027
Qy 1028 CTTTTGGCTCCAGTGGTTCATTTCTTTGTTAATCCCTTTTGTATCCATTTGTGTGTCACA 1087
Db 1028 CATTGCTGCTCAGTGGTTCATTTCTTTGTCATCTCTTTTGTATCCATTTGTGTGTCACA 1087
Qy 1088 AACGTTTTTCAGAGGCTTCTCTGAAATATCTTCTGTGAGAGGCAATTCACAGCCACCAC 1147
Db 1088 AGCGTTTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAAAGCAACCTCTACCATCAC 1147
Qy 1148 ACACCG 1154
Db 1148 AACACAG 1154

RESULT 13
US-10-417-820A-13
; Sequence 13: Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7, US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Query Match      57.7%; Score 675; DB 6; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACGATCGCCCTTAACATCAATTAATAATTTCTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCAATTTTATGTCCT 70

Qy 68 TACTAGCTATTGCTATATAGTGTAGGCAATGCTGGGTCAATTTAGCTTTTATTGTGACA 127
Db 71 TAGTAGCTTTTGTCTATATAGCTAGGAATGCTTTGGTCAATTTAGCTTTTGTGGTGACA 130

Qy 128 GAAATCTTAGACATCGAAGTAATTAATTTCTTAACTTTGGCCATTTGCACTTCTTTG 187
Db 131 AANAACCTTAGACATCGAAGTAGTATTATTTTCTTAACTTTGGCCATCTCTGACTTCTTTG 190

Qy 188 TGGGTGCAATTTGCAATTCCTCTGTACATACCTTTCTCGTGCCTGACTTACGACTTCTGGAA 247
Db 191 TGGGTGTGATCTCCATCTCTTTGTACATCCCTCACAGCTGTTCGAATGGGATTTTGGAA 250

Qy 248 AGCAAGCTTGTGATTTTGGCTCAATTAAGTACTGACTATTTTATGTPACAGCACTCTGTATA 307
Db 251 AGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTPACAGCACTCTGTATA 310

Qy 308 ATATTGCTCTCATCAGCTACGATCGCTACCACTGCTCAGTCTCAAAATGCGGTGTGTATAGAG 367
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Qy 368 CTCAGCACTTGGCACTGGAAATTTGCTACTAGATGGTGGCTGTGTGGATATCTCTCT 427
Db 371 CTCACACTTGGGCTCTTGAAGATTTGTTACTCTGATGGTGGCTGTGTGGTGTGGCT 430

Qy 428 TCATGACAAATGGGCGGATGTTCTGATTTTCAGACTCTTGGCAGATGAGCACTACAGAT 487
Db 431 TCTTAGTAATGGGCGGATGATTTCTAGTTTCAGAGTCTTGGAGGATGAGGATGAT 490

Qy 488 GTGAACCTGGATTTTAAAGTGGTACTTTGCTCTCCCTACATCAATTTTGAATTC 547
Db 491 GTGAACCTGGATTTTTCGGAATGGTATATCTCTTGGCATCATCATCTTCTGGAATTCG 550

Qy 548 TGATCCCATCTTGTGTAGTCTTATTTTCAGCGGCCCATATTTACTGGAGCTGTGGAGC 607
Db 551 TGATCCCATCTTCTTAGTCTTATTTTCAACATGAATATTTATTTGGAGCTGTGGAGC 610

Qy 608 GAGGAACTCAGCAGTGGCTCAGCCACCTGCTGACTCCCTGCTCTTCCAGCAGTG 667
Db 611 GTGATCATCTCAGTAGGTGCAAGGCCATCTGCACTGACTGCTGTCTTCCAAACA--- 667

Qy 668 ACCACGGACACTCTCTGACAGAGGACCCGATTCAGAGGCGACTCTGCGCAGCAGGAAG 727
Db 668 TCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGATCGACAG 727

Qy 728 AAACAATGCTCTCTTGGTTTCAGACAGTCAOOGGAGAAAGAGCAGTCTCTTGTTCCTCA 787
Db 728 AAGTTCCTGATCTCTTTCATTCAGAGAGACAGAGAGAGAGTAGTCTCATGTTTCTCT 787

Qy 788 TAAGGCTCAAGACAGCAATGATGCTGCTCCAAATGGGCTCTCTCTCCCACTCAG 847
Db 788 CAAGAACCAGATGAATAGCAATCAATTTGCTTCCAAATGGGTTCTCTCTCCCACTCAG 847

Qy 848 ATTCCCTGGCTCTTTCAGCAAGGGAACATATCGAACTTTTTCAGAGCCAGGAAATTAGCCA 907
Db 907
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RESULT 14
US-10-349-253A-1
; Sequence 1, Application US/10349253A
; Publication No. US20040043393A1
; GENERAL INFORMATION:
; APPLICANT: Aubart, Kelly
; APPLICANT: Bergema, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Graybill, Todd
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Morrow, Dwight
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C2
; CURRENT APPLICATION NUMBER: US/10/349,253A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/910,411
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-349-253A-1
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Query Match      57.7%; Score 675; DB 7; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;

Qy 8 CAAATACAGTACGATCGCCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCAATTTTATGTCCT 70

Qy 68 TACTAGCTATTGCTATATAGTGTAGGCAATGCTGGTCAATTTAGCTTTTATTGTGACA 127
Db 71 TAGTAGCTTTTGTCTATATAGTGTAGGAATGCTTTGGTCAATTTAGCTTTTGTGGTGACA 130

Qy 128 GAAATCTTAGACATCGAAGTAATTAATTTCTTAACTTTGGCCATTTGCACTTCTTTG 187
Db 131 AANAACCTTAGACATCGAAGTAGTATTATTTTCTTAACTTTGGCCATCTCTGACTTCTTTG 190

Qy 188 TGGGTGCAATTTGCAATTCCTCTGTACATACCTTTCTCGTGCCTGACTTACTGGAATTTCTGGAA 247
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Qy 308 ATATGTCTCTCATCAGCTACGATCGCTACCACTGATCTCAAAATGCGGTGTGTATAGAG 367
Db 311 ACATTTGCTCTCATCAGCTATGATGATACCTGTCAGTCTCAAAATGCTGTCTATAGAA 370
Qy 368 CTGACGACTCTGGCACTGGAAATGCTACTCAGATGGTGGCTGTTTGGATATCTCTCT 427
Db 371 CTCAACATACCTGGGCTCTTGAAGATTTGATCTGATGGTGGCGCTTTGGTGTGCGCT 430
Qy 428 TCATGACAAATGGGCCGATGATCTGATTTTCAGACTCTTGGCAGAAATGACACTACAGAA 487
Db 431 TCTTAGTGAATGGGCCAATGATCTAGTTTCAGAGTCTTGGAGGATGAAGGTAGTGAAT 490
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Db 491 GTGAACCTGGATTTTTCGGAATGGTACATCTCTTGGCCATCAGATCATCTTCTGGAATTC 550
Qy 548 TGATCCCATCTCTGTAGTTGCTTATTTTCAGCGCCCATATTTACTGAGCTGTGGGAAGC 607
Db 551 TGATCCCATCTCTGTAGTTGCTTATTTTCAGCGCCCATATTTACTGAGCTGTGGGAAGC 610
Qy 608 GAGAGAACTGAGCAGGTGCTTCAGCCACCTGATCTCCCTCTGACTCTTCCAGCAGTG 667
Db 611 GTGATCATCTCAGTAGTGGCCAAAGCCATCTCTGAGCTGATCTCTCTCCAAACA --- 667
Qy 668 ACCAGGACATCTCTGAGCAGAGACCCGATTCAGAGGGGAGTCTGCGCAGAGCGGAAAG 727
Db 668 TCTGTGACATCTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCACTCGACAG 727
Qy 728 AACAACCTGCTCTCTGTTTTCAGACAGTCAAGGAGAGAGAGAGTCTCTGTTTTCCTCA 787
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Qy 788 TAAGAGCTTCAAGAACAGCAATGTGATCGCTTCCAAATGGGCTCTCTCTCCCACTCAG 847
Db 788 CAAGAACCAAGATGAATAGCAATACATTTGCTTCCAAATGGGTTCTCTCTCCCACTCAG 847
Qy 848 ATTCCTGCTCTTTCAGAACAGGGAACATATCGAACTTTTCAGAGCCAGGAAATAGCCA 907
Db 848 ATCTGTAGCTCTTTCAGAACAGGGAACATATGAACTGCTTAGAGCCAGGAGATAGCCA 907
Qy 908 AGTCAGTGGCCATCTCTTAGCAGCTTTTGGCAATTTGCTGGGCTCCATATTCATGACTA 967
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Qy 1028 CTTTGTGGCTCCAGTGTTCATTTCTCTTGTATATCCCTTTTGTATCCATTTGTGTACAA 1087
Db 1028 CATTTTGGCTTCAGTGGTTCATTTCTCTTGTCAATCTCTTTTGTATCCATTTGTGTACAA 1087
Qy 1088 AACGTTTTCAGAGGCTTTTCTGAAATATCTTCTGTGAGAGGCAATTCACGCCACCAC 1147
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Qy 1148 ACAACCG 1154
Db 1148 AACACAG 1154
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RESULT 15

US-10-723-955-13

; Sequence 13, Application US/10723955

; Publication No. US20040110238A1

; GENERAL INFORMATION:

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; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lin, I-Lin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehman-Bruinsma, Karin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Gore, Martin
; APPLICANT: White, Carol
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; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

; FILE REFERENCE: 7 US29 CON

; CURRENT APPLICATION NUMBER: US/10/723,955

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 10/417,820

; PRIOR FILING DATE: 2003-4-16

; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: 60/110,060

; PRIOR FILING DATE: 1998-11-27

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,852

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/123,944

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,945

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,948

; PRIOR FILING DATE: 1999-03-12

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-723-955-13

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Query Match 57.7%; Score 675; DB 7; Length 1173;
Best Local Similarity 74.9%; Pred. No. 7.5e-185;
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;
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Qy 8 CAAATACAGTACAAATCGGCTTAAATCAATTAATTAATTTCTTTGACATTTTAAATGCTT 67
Db 11 CTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCATTTTATATGCTCT 70
Qy 68 TACTAGCTATGCTATAATGTTAGGCAATGCTGCTGTCATTTTAGCTTTTATTTAGTGACA 127
Db 71 TAGTACTTTTGTATAATGCTAGGAAATGCTTTTGTTCATTTTAGCTTTTGTGGTGACA 130
Qy 128 GAAATCTTAGACATCGAAGTAATTAATTTTCTTAATCTTGGCCATTTGACAGCTTCTTTG 187
Db 131 AAAACCTTAGACATCGAAGTAGTATTTTCTTAATCTTGGCCATCTCTGACTTCTTTG 190
Qy 188 TGGGTGCAATGCAATTCCTCTGTACATACCTTCCTCGCTGACTTACTGAGACTTCTGGAA 247
Db 191 TGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTTCGGAATGGGATTTGGAA 250
Qy 248 AGCAAGCTTGTGATTTTGGCTCATTTACTGACTATCTTTTATGTACAGCACTGTGTATA 307
Db 251 AGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCACTGTGTATA 310
Qy 308 ATATGTCTCTCATCAGCTACGATCGCTACCAAGTCAGTCTCAAAATGCGGTGTGTATAGAG 367
Db 311 ACATTTGCTCTCATCAGCTATGATCGATACCTGTCTGCTCAATGCTGTGTCTATAGAA 370
Qy 368 CTCAGCACTCTGGCACCTCGGAAATTTGCTACTACTCAGATGGTGGCTGTTTGGATATTCCTCT 427
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[illegible]

Search completed: April 30, 2006, 12:48:05  
Job time : 953 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2006, 14:40:24 ; Search time 375 Seconds  
(without alignments)  
5545.992 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170

Sequence: 1 atgttgcaataacagtac.....acgctcaatccacttga 1170

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	57.7	1173	3	US-09-414-010-1
2	675	57.7	1173	3	US-09-812-216-1
3	675	57.7	1173	3	US-09-875-076-13
4	132.2	11.3	1239	3	US-09-891-053-2
5	132.2	11.3	2700	3	US-09-891-053-5
6	123	10.5	1338	3	US-09-165-543-6
7	123	10.5	1953	3	US-09-891-053-26
8	123	10.5	3244	3	US-09-165-543-4
9	110.2	9.4	1335	2	US-08-985-090-3
10	110.2	9.4	1335	3	US-09-165-543-3
11	110.2	9.4	1335	3	US-09-167-354-6
12	110.2	9.4	1335	3	US-09-642-855-6
13	110.2	9.4	1335	3	US-09-642-514-6
14	110.2	9.4	1335	3	US-09-642-852-6
15	110.2	9.4	2050	3	US-09-891-053-21
16	110.2	9.4	2665	3	US-09-943-016-5059
17	110.2	9.4	2689	2	US-08-985-090-1
18	110.2	9.4	2689	3	US-09-165-543-1
19	110.2	9.4	2699	3	US-09-167-354-5
20	110.2	9.4	2699	3	US-09-642-855-5
21	110.2	9.4	2699	3	US-09-642-514-5
22	110.2	9.4	2699	3	US-09-642-852-5
23	83.2	7.1	1086	2	US-08-985-090-6
24	83.2	7.1	1086	3	US-09-165-543-33

25	83.2	7.1	2218	2	US-08-985-090-4	Sequence 4, Appli
26	83.2	7.1	2218	3	US-09-165-543-31	Sequence 31, Appli
27	73.4	6.3	1386	3	US-09-016-434-1339	Sequence 1339, Ap
28	73.4	6.3	1422	3	US-09-826-509-512	Sequence 512, App
29	73	6.2	1581	2	US-08-313-553-8	Sequence 8, Appli
30	73	6.2	1581	3	US-08-767-993-8	Sequence 8, Appli
31	73	6.2	1956	2	US-08-313-553-6	Sequence 6, Appli
32	73	6.2	1956	3	US-08-767-993-6	Sequence 6, Appli
33	71.2	6.1	1773	3	US-08-826-509-516	Sequence 516, App
34	71.2	6.1	1913	3	US-09-016-434-1314	Sequence 1314, Ap
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38	69.4	5.9	2210	3	US-10-166-199-1	Sequence 1, Appli
39	63.8	5.5	1599	3	US-09-826-509-520	Sequence 520, App
40	63.8	5.5	2261	3	US-09-016-434-1176	Sequence 1176, Ap
41	63.2	5.4	601	3	US-09-949-016-177027	Sequence 177027, Ap
42	63.2	5.4	1893	3	US-09-891-053-13	Sequence 13, Appli
43	63.2	5.4	9293	3	US-09-949-016-16801	Sequence 16801, A
44	55.4	4.7	1101	3	US-09-826-509-432	Sequence 432, App
45	55.4	4.7	1554	2	US-08-031-538-8	Sequence 8, Appli

#### ALIGNMENTS

RESULT 1  
US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monama, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

Query Match	57.7%	Score 675;	DB 3;	Length 1173;
Best Local Similarity	74.9%	Pred. No. 4.4e-203;		
Matches	859;	Conservative 0;	Mismatches 285;	Indels 3; Gaps 1;
Qy	8	CAATAACAGTACAAATCGCCCTTAACATCAATAAATTTCTTTGACATTTTAATGCTT	67	
Db	11	CTAATAGCAATCAATTTATCACTAGCACTCGTGTACTTTTAGCATTTTATGTCCT	70	
Qy	68	TACTAGCTATTGCTATTAATGTTAGGCAATGCGTGGTCAATTTTAGCTTTTATTTGGACA	127	
Db	71	TAGTAGCTTTTGGCTATTAATGCTAGGAATGCTTTGGTCATTTTAGCTTTTGGTGGACA	130	
Qy	128	GAATCTTTAGACATCGAAGTAATTAATCTTTTCTTAAGCTTGGCCATTCAGACTCTTTTG	187	
Db	131	AAACCTTAGACATCGAAGTAGTTATTTTCTTAAGCTTGGCCATCTCTGACTCTTTTG	190	
Qy	188	TGGTGGCAATTCCTCTGTACATACCTTCTCGCTGACTTACTTGGACTCTTGAA	247	
Db	191	TGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTGCAATGGGATTTTGGAA	250	
Qy	248	AGCAAGCTTGTTATTTGGCTCATCTACTGACTATCTTTTATGTACAGCATCTGTGATA	307	
Db	251	AGGAATCTGTGTTATTTTGGCTCACTACTGACTATCTGTATGTACAGCATCTGTATATA	310	





Db 788 CAAGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGTTCCTTCTCCCAATCAG 847  
Qy 848 ATTCCCTGGCTCTTCAGCAAAAGGGAACATATCGAACTTTTCAGAGCCAGGAAATTAGCCA 907  
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Qy 908 AGTCACCTGGCCATCTCTTACAGCTTTTGGCCATTTGCTGGGCTCCATATTCACCTGACTA 967  
Db 908 AGTCACCTGGCCATCTCTTGTAGGGGTTTGTGTGTGCTGGGCTCCATATTCCTGTTCAC 967  
Qy 968 CAGTTATCTACTCATTTTTTCTCGAAAGGAATTTGACTTAAATCAACCTGGTACCATACTG 1027  
Db 968 CAATTGCTCTTCAATTTTATTTCTCAGCAACAGGTCCTAATCATGTTGGTATAGAATTG 1027  
Qy 1028 CTTTTGGCTCCAGTGGTTCAATTCCTTGTGTAATCCCTTTTGTATCCATTTGTGTACACA 1087  
Db 1028 CAITTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTATCCATTTGTGTACACA 1087  
Qy 1088 AACGTTTTCAAGAGCTTTTCTCGAAATPACTTCTGTGAGAGGCAATCCACGCCACCAC 1147  
Db 1088 AGCGCTTCAAAGGCTTCTTGAAATATTTTGTATATAAAAGCAACCTCTACCATCAC 1147  
Qy 1148 ACAACCG 1154  
Db 1148 AACACAG 1154

## RESULT 3

US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Patent No. 6869776  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
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; PRIOR APPLICATION NUMBER: 60/136,439  
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; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
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; PRIOR FILING DATE: 1999-09-29  
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; PRIOR FILING DATE: 1999-09-29  
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; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
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; PRIOR APPLICATION NUMBER: 60/157,281  
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; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-076-13  
  
Query Match 57.7%; Score 675; DB 3; Length 1173;  
Best Local Similarity 74.9%; Pred. No. 4.4e-203;  
Matches 859; Conservative 0; Mismatches 285; Indels 3; Gaps 1;  
  
Qy 8 CAAATAACAGTACCAATCGCCTTAACATCAATTAATAATTTCTTTGACATTTTAAATGCTT 67  
Db 11 CTAATAGCACAAATCAATTTTATCATAAGCACTCGTGTACTTTAGCAATTTTATGTCT 70  
  
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Db 251 AGGAAATCTGTATATTTTGGCTCACTGACTATCTGTTATGTACAGCATCTGTATATA 310  
  
Qy 308 ATATTGCTCATCAGCTACGATCGTACCATGCTCAGTCTCAATGCGGTGGTGTATAGAG 367  
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Qy 368 CTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTTGGATATTTCTCT 427  
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Qy 488 GTGAACCTGGATTTTAAAGATGTTGCTCTCCCTACATCATTTTGAATTTCC 547  
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APPLICANT: Takimura, Tetsuo  
APPLICANT: Nakamura, Takao  
APPLICANT: Kobayashi, Masahiko  
APPLICANT: Tanaka, Ken-ichi  
APPLICANT: Hidaka, Yusuke  
APPLICANT: Ohta, Masataka  
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
FILE REFERENCE: 06501-083001  
CURRENT APPLICATION NUMBER: US/09/891,053  
CURRENT FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: PCT/JP99/07280  
PRIOR FILING DATE: 1999-12-24  
PRIOR APPLICATION NUMBER: PCT/JP98/05967  
PRIOR FILING DATE: 1998-12-25  
PRIOR APPLICATION NUMBER: JP 11/145661  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 2700  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (351)...(1589)  
NAME/KEY: misc feature  
LOCATION: (1)...(2700)  
OTHER INFORMATION: n = A,T,C or G  
US-09-891-053-5

Query Match 11.3%; Score 132.2; DB 3; Length 2700;  
Best Local Similarity 48.7%; Pred. No. 7.3e-31;  
Matches 523; Conservative 0; Mismatches 528; Indels 24; Gaps 5;

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Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACCTGGCCATTGCAG 178  
Db |||||  
Qy 529 TGGCGGATTCAGGCTCCGCCACAGAACAACTTTCTTGCTCAACTCGCCATCTCG 588  
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Qy 179 ACTTCTTTGGGGTGCAATGCAATCTCTCTGTAATACATCTTCTCTGCTGCTGCTGCTTAC---T 235  
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Qy 589 ACTTCTCTGGTGGCTCTCTGCAATGTCATCCCAATGTAAGTACCTATGTCGACCGCGGTT 648  
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Qy 236 GGACTTCTGGAAGCAAGCTTGTAATTTGGCTCATTAATGCTACTGATATCTTTTATGTACAG 295  
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Qy 649 GGACCTTTCGGCCGGGCGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTACTGTGTGCT 708  
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Qy 296 CATCTGTATAATATTTCTCTCATCAGCTACGATCGCTACGCTCAGTCTCAAAATGCG 355  
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Qy 356 TGTGGTATAGAGCTCAGCACTCTGGCACCTGGCAAAATGCTACTCAGATGGTGGCTGTT 415  
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Qy 416 GGATAATCTCTTCAATGCAAAATGGGCGATGATCTGATTTTCACTCTTGGCAGATA 475  
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Qy 476 GCCTACAG-----AATGTGAACCTGGAATTTTAAAGATGGTACTTTTGTCT 523  
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Qy 889 GCAGTTCAATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACACTGGTACTTTCTCA 948  
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Qy 524 TCCCTACATCATTAATGGAATTCCTGATCCCAATCTTTGTTAGTTGCTTAATTCAGCGCCC 583  
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Qy 949 TCAGGGCTCCACCTCGAGTTCTTCAGCGCCCTTCTCAGGTTTACCTTCTTCAACTCA 1008  
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Qy 584 ATATTACTGAGGCTGTGGAGCGAGAGAACTGAGCAGGTGCTCAGCCACCTGTAC 643  
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Db 1009 GCATCTACTGAACATCCAGAGGCGCACCCTTTCGGCTTGTATGGGGCCGTGAGGCTG 1068  
Qy 644 TCCCTCTGACTCTTCCAGAGTGAACACGAGCACTCTCTGAGACAGAGACCCCGATTCAA 703  
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Db 1069 GCCAGGAACC-----CCACCAGATGCCAGCCCTCGCCACCTCCAGCTTCCCGCCAGCTGC 1124  
Qy 704 GGGGACTCTGCGCAGCAGGGAAGAAACACTGCTCTCTTGGTTTCAGACAAGTCAACGGA 763  
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Db 1125 TGGGGCTGTGGCCAAAGGGCATGGGAGGCCATGCGCTTGGCAGCTCTGGGAGCTCC 1184  
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Db 1303 TGTGCGGGACAAGAGGTGGCCAAAGTGGTGGCCATCATCGTGAAGCATCTTTGGGCTCT 1362  
Qy 944 GCTGGGCTCCATATTCCTGACTACAGTATCTACTCATTTTCTTCTGAAAGGAATTTGA 1003  
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Db 1480 CCGTCTCTTACCCACTGTGCCACTACAGCTTCGCGAGGCTTCACCAAGCTCT 1534

RESULT 6  
US-09-165-543-6  
; Sequence 6, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1338 base pairs  
; TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1335  
US-09-165-543-6

Query Match 10.5%; Score 123; DB 3; Length 1338;  
Best Local Similarity 54.0%; Pred. No. 3.9e-28;  
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;  
QY 59 TAATGCTCTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTAGCTTTTA 118  
Db 119 TCATGGCGCTGCTCATCTGGCCACAGTACTGGGCAACGGCTGCTCATGCTGCCCTTCG 178  
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACCTGGCCATTGCG 178  
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QY 179 ACTTCTTTGGGTGGCAATGCAATTCCTCTGTACATACCTTCTCGCTCACTTAC---T 235  
Db 239 ACTTCTCTGGGTGGCTTCTGCAATCCCATTTGTACGTACCTATGCTGACCGGCGGTT 298  
QY 236 GGAATCTCTGAAAGCAAGCTTGTTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAG 295  
Db 299 GGAATCTCTGGCGGGGCTCTGCAAGCTTGCTGGTGGTAGACTACTTACTGTGCTT 358  
QY 296 CATCTGTGTATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCACTTCAAAATGCCG 355  
Db 359 CCTGGGTCTTCAACATCGTACTCATCAGTATGACCGAATTCCTGTCACTCACTCGAGCTG 418  
QY 356 TGTGTTATAGAGCTCAGCAGCTCTGGACCTGGAAATGTTGCTACAGATGGTGGCTGTTT 415  
Db 419 TCTCTACAGGGCCAGCAGGGGACACGAGACGGGCGCTTCCGAAGATGGCACTGGTGT 478  
QY 416 GGAATTTCTCTTCATCAGAAATGGGCGGATGTTCTGATTTTCAGACTCTTTGGCAGAATA 475  
Db 479 GGGTGTGGCTTCTCTGTATGGGCTGCTGCAATCTTCACTTGGAGTACTCTGTCTGGTG 538  
QY 476 GCACTACAG-----AATGTGAACCTGGATTTTAAAGTGGTACTTTGCTC 523  
Db 539 GCAATTCATCCCGAGGGGCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCA 598  
QY 524 TCCCTACATCATTAATTTGGAATTCCTGATCCCATCTTGTAGTGTCTTATTTACGGCCC 593  
Db 599 TCAGGGCTCCACCTCGAGTTCTTACGGCCCTTCTCAGCGCTTCTCAGCGTTTACCTTCTCAACCTCA 658  
QY 584 ATATTACTGGAGCTCTGGAAGCG 608  
Db 659 GCATCTACCTGAACATCCAGAGCG 683

## RESULT 7

US-09-891-053-26

Sequence 26, Application US/09891053

Patent No. 6750322

GENERAL INFORMATION:

APPLICANT: Itadani, Hiraku

APPLICANT: Takimura, Tetsuo

APPLICANT: Nakamura, Takao

APPLICANT: Kobayashi, Magahiko

APPLICANT: Tanaka, Ken-ichi

APPLICANT: Hidaka, Yusuke

APPLICANT: Ohta, Masataka

TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

FILE REFERENCE: 06501-083001

CURRENT APPLICATION NUMBER: US/09/891,053

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: PCT/JP99/07280

PRIOR FILING DATE: 1999-12-24

PRIOR APPLICATION NUMBER: PCT/JP98/05967

PRIOR FILING DATE: 1998-12-25  
PRIOR APPLICATION NUMBER: JP 11/145661  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 1953  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (302)...(1636)  
US-09-891-053-26

Query Match 10.5%; Score 123; DB 3; Length 1953;  
Best Local Similarity 54.0%; Pred. No. 4.9e-28;  
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;  
QY 59 TAATGCTCTTACTAGCTATTGCTATAATGTTAGGCAATGCTGGTCAATTTAGCTTTTA 118  
Db 420 TCATGGCGCTGCTCATCTGGCCACAGTACTGGGCAACGGCTGCTCATGCTGCCCTTCG 479  
QY 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACCTGGCCATTGCG 178  
Db 480 TGGCGGATTTCGAGCTCCGACCCAGAACTTCTTTCTGCTCAACCTGCCATCTCCG 539  
QY 179 ACTTCTTTGGGTGGCAATGCAATTCCTCTGTACATACCTTCTCGCTCACTTAC---T 235  
Db 540 ACTTCTCTGGGTGGCTTCTGCAATCCCATTTGTACGTACCTATGCTGACCGGCGGTT 599  
QY 236 GGAATTTCTGAAAGCAAGCTTGTTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAG 295  
Db 600 GGAATTTCTGGCGGGGCTCTGCAAGCTTGCTGGTGGTAGACTACTTACTGTGCTT 659  
QY 296 CATCTGTGTATAATTTGCTCTCATCAGCTACGATCGCTACCAAGTCACTTCAAAATGCCG 355  
Db 660 CCTGGGTCTTCAACATCGTACTCATCAGCTATGACCGAATTCCTGTCACTCACTCGAGCTG 719  
QY 356 TGTGTTATAGAGCTCAGCAGCTCTGGACCTGGAAATGTTGCTACAGATGGTGGCTGTTT 415  
Db 720 TCTCTACAGGGGCGGCGGACACGAGACGGGCGGTTCCGAAGATGGCACTGGTGT 779  
QY 416 GGAATTTCTCTTCATGACAAATGGGCGGATGTTCTGATTTTCAGACTCTTTGGCAGAATA 475  
Db 780 GGGTGTGGCTTCTCTGCTGTAATGGGCTGCCATCTGAGTTGGAGTACTCTGTCTGGTG 839  
QY 476 GCACTACAG-----AATGTGAACCTGGATTTTAAAGTGGTACTTTGCTC 523  
Db 840 GCAATTTCCATCCCGAGGGGCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCA 899  
QY 524 TCCCTACATCATTAATTTGGAATTCCTGATCCCATCTTGTAGTGTCTTATTTACGGCCC 583  
Db 900 TCAGGGCTCCACCTCGAGTTCTTACGGCCCTTCTCAGCGCTTCTCAGCGTTTACCTTCTCAACCTCA 959  
QY 584 ATATTACTGGAGCTCTGGAAGCG 608  
Db 960 GCATCTACCTGAACATCCAGAGCG 984

## RESULT 8

US-09-165-543-4

Sequence 4, Application US/09165543

Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann

TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE &amp; COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA



Qy	356	TGTTGTTATAGAGCTCAGCACTCTGGCACCTGGAAAAATTGCTACTCAGATGGTGGCTGTTT	415
Db	419	TCTCATACCGGGCCAGCAGGGTGACACGGGGGAGTGGCGAAGATGCTGCTGCTGT	478
Qy	416	GGATATTCTCTTCATGACAAAATGGGCGGATGATTTCTGATTTTCAAGCTCTTGGCAGAAATA	475
Db	479	GGGTGCTGGGCTTCTCTGTATACGACACAGCCATCTCTGAGCTGGGAGTACCTGTCCGGGG	538
Qy	476	GCCTAC-----AGAAATGTAACCTGGATTTTAAAAAGTGGTACTTTGCTC	523
Db	539	GCAGCTCCATCCCGAGGGCCACTGTCGCGAGTTCCTTCAACCTGGTACTTCTCA	598
Qy	524	TCCCTACATCAATTATTGGAATTCCTGATCCCACTTTGTTAGTTGCTTAFTTCAGGCGCC	583
Db	599	TCAGGCTTCCACCTCGAGTTCTTTACGCCCTTCTCAGCGTCACTCTTTAACTCA	658
Qy	584	ATATTACTGGAGCTGTGGAAGCG	608
Db	659	GCATCTACCTGAACATCCAGAGCG	683
RESULT 10			
US-09-165-543-3			
; Sequence 3, Application US/09165543			
; Patent No. 6093545			
; GENERAL INFORMATION:			
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann			
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor			
; NUMBER OF SEQUENCES: 39			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: LAHIVE & COCKFIELD, LLP			
; STREET: 28 State Street			
; CITY: Boston			
; STATE: Massachusetts			
; COUNTRY: USA			
; ZIP: 02109			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/165,543			
; FILING DATE:			
; CLASSIFICATION:			
; PRIORITY APPLICATION DATA:			
; APPLICATION NUMBER: 09/042,780			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Elizabeth A. Hanley			
; REGISTRATION NUMBER: 33,505			
; REFERENCE/DOCKET NUMBER: MNI-032CP			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617)227-7400			
; TELEFAX: (617)742-4214			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1335 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: CDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 1..1335			
US-09-165-543-3			
Query Match 9.4%; Score 110.2; DB 3; Length 1335;			
Best Local Similarity 52.6%; Pred. No. 4.5e-24;			
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;			
Qy	59	TAATGCTTTTACTAGCTATTGCTATATATGTTAGGCAATGTCGTGGTCAATTTTACTGCTTTTA	118

Db	119	TCATGGCGTCTCATCTGGCCACGCTGTGGGCAACGCGTGTCTATGCTCGCCTTCG	178
Qy	119	TTCTGGACAGAAATCTTAGACATCGAAGTAATTTACTTTTTTCTTAATCTGGCCATTCGAG	178
Db	179	TGCCGACTCGAGCCTCCGCAACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCG	238
Qy	179	ACTTCTTTTGTGGTGCAATTGCAATTCTCTGTATACATACCTTCTCTCGCTGAC---TTACT	235
Db	239	ACTTCTCTGTCGGCGCTTCTGCAATCCACTGTATGTACCTAGGTGCTGACAGGCGCT	298
Qy	236	GGACTTCTGGAAGCAAGCTTGTGTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAG	295
Db	299	GGACCTTTCGGCCGGGCTCTGCAAGCTGTGGTGGTAGTGGACTACTCTGTGTGCACT	358
Qy	296	CATCTGTGTATATATTGTCTCATCAGCTACCATCGCTACAGTCAAGTCTCAAAATGCGG	355
Db	359	CCTCTGCTTCAACATCGTGTCTCATCAGCTACCAACGCTTCTGTGTCGTCACCCGAGCGG	418
Qy	356	TGTGTATATAGAGCTCAGCACTCTGGCACCTTGCGAAAAATTGCTACTCAGATGGTGGCTGTTT	415
Db	419	TCTCATACCGGGCCAGCAGGGTGACACGGCGGGCAGTGGCGAAGATGCTGCTGTGT	478
Qy	416	GGATATTCTCTTCATGACAAAATGGGCGGAGATTTCTGATTTTCAAGTCTTTGGCAGAAATA	475
Db	479	GGGTGCTGGCTTCTCTGTGTATACGACACAGCCATCTCTGAGCTGGGAGTACTCTGTCCGGGG	538
Qy	476	GCACTAC-----AGAAATGTAACCTGGATTTTAAAAAGTGGTACTTTGCTC	523
Db	539	GCAGCTCCATTCGCCGAGGGCCACTGCTATGCCGAGTTCCTTCAACCTGGTACTTCTCA	598
Qy	524	TCCCTACATCAATTATTGGAATTCCTGATCCCACTTTGTTAGTTGCTTAFTTCAGGCGCC	583
Db	599	TCAGGCTTCCACCTCGAGTTCTTTACGCCCTTCTCAGCGTCACTCTTTAACTCA	658
Qy	584	ATATTACTGGAGCTGTGGAAGCG	608
Db	659	GCATCTACCTGAACATCCAGAGCG	683
RESULT 11			
US-09-167-354-6			
; Sequence 6, Application US/09167354A			
; Patent No. 6136559			
; GENERAL INFORMATION:			
; APPLICANT: Lovenberg, Timothy			
; APPLICANT: Erlander, Mark			
; APPLICANT: Pyati, Jayashree			
; APPLICANT: Huvar, Arne			
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3			
; FILE REFERENCE: SUBTYPE			
; CURRENT APPLICATION NUMBER: US/09/167,354A			
; CURRENT FILING DATE: 1998-10-07			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 6			
; LENGTH: 1335			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:CDNA			
US-09-167-354-6			
Query Match 9.4%; Score 110.2; DB 3; Length 1335;			
Best Local Similarity 52.6%; Pred. No. 4.5e-24;			
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;			
Qy	59	TAATGCTTTTACTAGCTATTGCTATATATGTTAGGCAATGTCGTGGTCAATTTTACTGCTTTTA	118
Db	119	TCATGGCGTCTCATCTGGCCACGCTGTGGGCAACGCGTGTCTATGCTCGCCTTCG	178
Qy	119	TTCTGGACAGAAATCTTAGACATCGAAGTAATTTACTTTTTTCTTAATCTGGCCATTCGAG	178



Db 179 TGGCGAGCTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCG 238  
Qy 179 ACTTCTTTGGGTGGGTAATGGAATTCCTCTGTATACATACCTTCTCGCTGAC---TTACT 235  
Db 239 ACTTCTCGTGGGGCCCTTCTGCAATCCACATGATATACCTAGCTGTGACAGGCCGCT 298  
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295  
Db 299 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGTGTGCACCT 358  
Qy 296 CATCTGTGTATAATATTTCTCTCATCAGTACGATCGCTACAGTCACTCTCAAAATGCG 355  
Db 359 CCTCTGCTTCAACATCTGTCTCATCAGTACGACCGCTTCTGTGTGTGACCGAGGG 418  
Qy 356 TGTGGTATAGAGCTCAGACACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGTGTTT 415  
Db 419 TCTCATACCGGGCCAGCAGGCTGACACGCGCGGCGAGTGGGAAGATGCTGTGTGT 478  
Qy 416 GGATATTCTCTCATGACAAATGGCGGATGATTTCTGATTTTCTGAGCTCTTGGCAGATA 475  
Db 479 GGGTGTGGCTTCTCTGTACGACCGACCATCTCTGAGCTGGGAGTACCTGTCCGGGG 538  
Qy 476 GCACTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGGTACTTTTGTCT 523  
Db 539 GCAGCTCAATCCCGAGGGCCACTGTATGCGAGTCTTCTACAACTGGTACTTCTCTCA 598  
Qy 524 TCCCTACATCAATATGGAATTCCTGATPCCCATCTTGTGTAGTGTCTTATTTACGCGCC 583  
Db 599 TCAGGGCTTCCACCTGGAGTCTTTAGCGCTTCTCTCAGCGTCACTTCTTTAACTCA 658  
Qy 584 ATATTACTGGAGCTGTGGAAGCG 608  
Db 659 GCATCTACCTGAACATCCAGAGCG 683

## RESULT 12

US-09-642-855-6  
; Sequence 6, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR FILING DATE: 09/167,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-642-855-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;  
Best Local Similarity 52.6%; Pred. No. 4.5e-24;  
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;  
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGTGCTATTTAGCTTTTA 118  
Db 119 TCATGGCGCTCTCATCTGGCCACGGTGTGGGCAAGCGCTGTATGCTCGCTTCG 178  
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCATTGCG 178  
Db 179 TGGCCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCG 238

Qy 179 ACTTCTTTGGGTGGGTAATGGAATTCCTCTGTATACATACCTTCTCGCTGAC---TTACT 235  
Db 239 ACTTCTCGTGGGGCCCTTCTGCAATCCACATGATATACCTAGCTGTGACAGGCCGCT 298  
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295  
Db 299 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGTGTGCACCT 358  
Qy 296 CATCTGTGTATAATATTTCTCTCATCAGTACGATCGCTACAGTCACTCTCAAAATGCG 355  
Db 359 CCTCTGCTTCAACATCTGTCTCATCAGTACGACCGCTTCTGTGTGTGACCGAGGG 418  
Qy 356 TGTGGTATAGAGCTCAGACACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGTGTTT 415  
Db 419 TCTCATACCGGGCCAGCAGGCTGACACGCGCGGCGAGTGGGAAGATGCTGTGTGT 478  
Qy 416 GGATATTCTCTCATGACAAATGGCGGATGATTTCTGATTTTCTGAGCTCTTGGCAGATA 475  
Db 479 GGGTGTGGCTTCTCTGTACGACCGACCATCTCTGAGCTGGGAGTACCTGTCCGGGG 538  
Qy 476 GCACTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGGTACTTTTGTCT 523  
Db 539 GCAGCTCAATCCCGAGGGCCACTGTATGCGAGTCTTCTACAACTGGTACTTCTCTCA 598  
Qy 524 TCCCTACATCAATATGGAATTCCTGATPCCCATCTTGTGTAGTGTCTTATTTACGCGCC 583  
Db 599 TCAGGGCTTCCACCTGGAGTCTTTAGCGCTTCTCTCAGCGTCACTTCTTTAACTCA 658  
Qy 584 ATATTACTGGAGCTGTGGAAGCG 608  
Db 659 GCATCTACCTGAACATCCAGAGCG 683

## RESULT 13

US-09-642-514-6  
; Sequence 6, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: ORT1290  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR FILING DATE: 09/167,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:CDNA  
US-09-642-514-6

Query Match 9.4%; Score 110.2; DB 3; Length 1335;  
Best Local Similarity 52.6%; Pred. No. 4.5e-24;  
Matches 297; Conservative 0; Mismatches 253; Indels 15; Gaps 2;  
Qy 59 TAATGCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGTGCTATTTAGCTTTTA 118  
Db 119 TCATGGCGCTCTCATCTGGCCACGGTGTGGGCAAGCGCTGTATGCTCGCTTCG 178  
Qy 119 TTGTGGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCATTGCG 178  
Db 179 TGGCCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCG 238  
Qy 179 ACTTCTTTGGGTGGGTAATGGAATTCCTCTGTATACATACCTTCTCGCTGAC---TTACT 235

239	ACTTCCTCGTCGGCGCCTTCGTCATCCCACTGTATGTACCTCATCGTGTGACAGCGCGCT	298
236	GGACTTCTGGAAAGCAAGCTTGTGTATTTTGGCTCATTACTGACTATCTTTTATGTACAG	295
299	GGACCTTCGGCGCGGGCGCTCTGCAAGCTGTGGCTGCTAGTGGACTACCTCTGCTGTGCACCT	358
296	CATCTGTGTATAATAATTGTCTCATCAGCTACGATCGCTACCGAGTCAGTCTCAAAATGCCG	355
359	CCTCTGCCCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTCTGGTCACTCCGAGCGG	418
356	TGTGGTATPAGAGCTCAGCACTCTGGCACCTGGCAAAATTGCTACTCAGATGGTGGCTGTTT	415
419	TCTCATACCGGGCCGACGCGGTGACACGCGCGGGCAGTGGCGGAAGATGCTCTGTGGTGT	478
416	GGATATTCCTCTTCATGACAAATGGCGCGGATGATTCGTATTTCAGACTCTTGGCAGAATA	475
479	GGGTGCTGGCCTTCTCTGTGTACGGACCAAGCCATCTGAGCTGGGAGTACCTGTCCGGGG	538
476	GCACCTAC-----AGAACTGAACCTGGATTTTTTAAAAAAGTGGTACTTTGCTC	523
539	GCAGCTCCATCCCCGAGGGCCACTGCTATGCGAGTTCTTCTACAACCTGGTACTTCTCCTCA	598
524	TCCCTACATCATTAATGGAAATTCCTGATCCCATCTGTGTAGTGTGCTTATTTTCAGCGCC	583
599	TCACGGCTTCCACCTGGAGTTCCTTACGCCCTTCTCCTCAGCGTCACCTCTTTAACCTCA	658
584	ATATTTACTGGAGCCTGTGGAGCG	608
659	GCATCTACTGAACATCCAGAGGCG	683

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RESULT 14
US-09-642-852-6
; Sequence 6, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JWJ
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-642-852-6

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Query Match	9.4%;	Score 110.2;	DB 3;	Length 1335;
Best Local Similarity	52.6%;	Pred. No. 4.5e-24;		
Matches 297;	Conservative 0;	Mismatches 253;	Indels 15;	Gaps 2;
Qy	59	TAATGTCCTTTACTAGCTATTGCTATATGTTTGGGCAATGTCGTGCTCATTTTAGCTTTTA	118	
Db	119	TCATGGCGCTGCTCATGTCGTGCCACGGTCTGGGCAACGGCGCTGGTATGCTCGCCTTCG	178	
Qy	119	TTGTGGACAGAAATCTTAGACATCGAAGTAAATTACTTTTTTCTTAACTTGGCCATTGCAG	178	
Db	179	TGGCCGACTCGAGCCTCGGACCCGAGAACAACCTTCTTCTGCTCAACTCGCCATCTCCG	238	
Qy	179	ACTTCTTTTGGGGTGCAATTGCAATTCCTCTGTGATCATACCTTCTCTCGGTGAC---TTACT	235	
Db	239	ACTTCTCGTCGGCGCCCTTCTGCATCCCACTGTATGACCTGATGTCAGTCGTGTGACGGCGCT	298	

Qy	236	GGACTTCTGGAAAGCAAGCTTGTGTAATTTTGGCTCATTTACAGACTATCTTTTATGTACAG	29
Db	299	GGACTTCTGGCCGGGGCCCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACCT	358
Qy	296	CATCTGTGTATAATTTGTCTCATACAGTACAGATCGCTACAGTCAAGTCTCAAATGCGG	355
Db	359	CTCTGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCGTCAACCGAGCGG	418
Qy	356	TGTGGTATPAGAGCTCAGCACCTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTT	415
Db	419	TCTCATACCGGGCCACAGCGGTGACACGCGCGCGGAGTGGGAAGATGCTGCTGGTGT	478
Qy	416	GGATATTCTCTTCAATGACAAATGGCGCGATGATTTCTGATTTACAGACTCTTGGCAGAAAT	475
Db	479	GGGTGCTGGCCCTTCTGTGTACGGAACAGCCATCTGAGCTGGGAGTACCTGTCCGGGG	538
Qy	476	GCATAC-----AGAACTGGAACCTGGGATTTTAAAAAGTGGTACTTTGCTC	523
Db	539	GCAGCTCAATCCCGAGGGCCACTGCTATGCGAGTCTTTCTACACTGGTACTTCTCTCA	598
Qy	524	TCCCTCATCATTAATTGGAAATTCCTGATCCCATCTTGTAGTTCGTTATTTTACAGCGCC	583
Db	599	TACGGCTTCCACCTTGGAGTTCCTTAGCGCCCTCCTCAGCGTCACTTCTTTAACCCTCA	658
Qy	584	ATATTTACTGGAGCCTGTGGAGCG	608
Db	659	GCATCTACCTGAACATCCAGAGGG	683

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RESULT 15
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent NO. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271) ... (1629)
US-09-891-053-21

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	Query Match	9.4%	Score 110.2;	DB 3;	Length 2050;
	Best Local Similarity	52.6%;	Pred. No. 5.8e-24;		
	Matches 297;	Conservative 0;	Mismatches 253;	Indels 15;	Gaps 2;
Qy	59	TAATGCTTTTACTAGCTATTGCTATATATGTTAGGCAATGTCGTGTCATTTTAGCTTTTA	118		
Db	389	TCATGGCGCTGCTCATCGTGCACAGGTCTGGCAACGGCGTGGTCATGCTCGCCTTCG	448		
Qy	119	TTTGGGACAGAAATCTTATGACATCGAAGTAATTACTTTTCTTACTTGCCCATTCGAG	178		

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Db 449 TGGCGGACTCGAGCCTCGCACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCG 508
Qy 179 ACTTCTTTGTGGGTGCAATTCTCTGTACATACCTTCTCTGCTGAC---TTACT 235
Db 509 ACTTCTCTGTGCGGCGCTTCTGCAATCCCACTGTATGTATACCTGTGCTGACAGGCGCT 568
Qy 236 GGACTTCTGGAAAGCAAGCTTGTGTATTTTGGCTCATTTACTGACTATCTTTTATGTACAG 295
Db 569 GGACTTCTGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACTGTGTGCACCT 628
Qy 296 CATCTGTGTATAATATTGTCTCTATCAGTACGATCGCTACAGTCTCAAAATGCCG 355
Db 629 CCTCTGCCCTTCAACATCGTGTCTATCAGTACGACCGCTTCTGTGCTCACCCGAGCGG 688
Qy 356 TGTGGTATAGAGCTCAGCACTCTGGCACCTCGAAATTTGCTACTCAGATGCTGCTGTTT 415
Db 689 TCTCATACCGGGCCCGACGAGGTGACACGCGCGCGGCGAGTCCGGAAGATGCTGCTGTGT 748
Qy 416 GGATATTCTCTTCATGACAAATGGCGGATGATTCTGATTTTCAGACTCTTTGGCAGAATA 475
Db 749 GGGTGTGGCCCTTCTGTGTACGACCGACCCATCTGAGCTGGAGTACCTGTCCGGGG 808
Qy 476 GCACTAC-----AGAAATGTGAACCTGGATTTTAAAAAGTGTACTTTGCTC 523
Db 809 GCAGCTCATCCCGAGGGCCACTGCTATGCGAGTTCTTCTACAACTGGTACTTCTCTCA 868
Qy 524 TCCCTACATCATATTATGGAATTCCTGATCCCCATCTGTGTAGTTGCTTATTTCAAGCGCC 583
Db 869 TCAGGGCTTCCACCGCTGGAGTTCCTTAGCCCTTCTCAGCGTCACTTCTTTAACCTCA 928
Qy 584 ATATTACTGGAGCTGTGGAGCG 608
Db 929 GCATCTACCTGAACATCCAGAGCG 953
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Search completed: April 29, 2006, 14:52:09  
Job time : 379 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2006, 23:57:16 ; Search time 625 Seconds  
(without alignments)  
7602.696 Million cell updates/sec

Title: US-10-626-398-7

Perfect score: 1170

Sequence: 1 atgttgcaataacagctac.....acggctcaataccacttga 1170

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9295968 seqs, 2030634719 residues

Total number of hits satisfying chosen parameters: 18591936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

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- 2: /SIDSS/ptodata/2/pubpna/US06 NEW PUB.seq.\*
- 3: /SIDSS/ptodata/2/pubpna/US07 NEW PUB.seq.\*
- 4: /SIDSS/ptodata/2/pubpna/PCT NEW PUB.seq.\*
- 5: /SIDSS/ptodata/2/pubpna/US09 NEW PUB.seq.\*
- 6: /SIDSS/ptodata/2/pubpna/US09 NEW PUB.seq.\*
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- 9: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq.\*
- 10: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq.\*
- 11: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq.\*
- 12: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq.\*
- 13: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq.\*
- 14: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq.\*
- 15: /SIDSS/ptodata/2/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	270	23.1	1326	14	US-11-241-956-19 Sequence 19, Appl
2	123	10.5	2761	11	US-11-036-196-2003 Sequence 2003, Ap
3	123	10.5	2814	14	US-11-136-527-3990 Sequence 3990, Ap
4	117.4	10.0	2824	14	US-11-136-527-127 Sequence 127, App
5	72.6	6.2	2483	14	US-11-136-527-2847 Sequence 2847, Ap
6	72.4	6.2	2633	14	US-11-136-527-3114 Sequence 3114, Ap
7	71.2	6.1	1773	14	US-11-127-877-17 Sequence 17, Appl
8	71.2	6.1	1974	14	US-11-124-368A-14 Sequence 14, Appl
9	71	6.1	2348	11	US-11-136-527-3691 Sequence 3691, Ap
10	71	6.1	3578	11	US-11-036-196-1495 Sequence 1495, AD
11	71	6.1	4095	14	US-11-136-527-2030 Sequence 2030, Ap
12	69.4	5.9	1401	14	US-11-127-877-4 Sequence 4, Appli
13	68.4	5.8	2733	14	US-11-136-527-2435 Sequence 2435, Ap
14	63.8	5.5	2699	14	US-11-127-877-5 Sequence 5, Appli
15	53.8	4.6	3741	14	US-11-136-527-751 Sequence 751, App
16	53	4.5	2591	14	US-11-136-527-1944 Sequence 1944, Ap
17	52.6	4.5	2146	8	US-10-750-185-35936 Sequence 35936, A
18	52.6	4.5	2146	8	US-10-750-623-35936 Sequence 35936, A

19	51	4.4	1020	14	US-11-127-877-12	Sequence 12, Appl
20	51	4.4	1020	14	US-11-174-816-2	Sequence 2, Appli
21	51	4.4	1038	11	US-11-217-710-5	Sequence 5, Appli
22	50.6	4.3	1496	14	US-11-136-527-2608	Sequence 2608, Ap
23	49.8	4.3	85980	11	US-11-114-798-46	Sequence 46, Appl
24	49.8	4.3	197241	11	US-11-114-798-47	Sequence 47, Appl
25	49.4	4.2	1020	14	US-11-174-751-2	Sequence 2, Appli
26	45.8	3.9	1768	14	US-11-136-527-2121	Sequence 2121, Ap
27	44.8	3.8	1030	14	US-11-174-816-6	Sequence 6, Appli
28	44.8	3.8	1032	14	US-11-174-816-7	Sequence 7, Appli
29	44.8	3.8	1032	14	US-11-174-816-71	Sequence 71, Appl
30	44.8	3.8	1032	14	US-11-174-819-90	Sequence 90, Appl
31	44.8	3.8	1032	14	US-11-174-751-41	Sequence 41, Appl
32	44.8	3.8	1435	8	US-10-750-185-26145	Sequence 26145, A
33	44.8	3.8	1435	8	US-10-750-623-26145	Sequence 26145, A
34	44.2	3.8	2509	14	US-11-136-527-3738	Sequence 3738, Ap
35	43.4	3.7	1047	14	US-11-174-819-33	Sequence 33, Appl
36	42.6	3.6	1400	14	US-11-136-527-4223	Sequence 4223, Ap
37	42.6	3.6	1400	14	US-11-136-527-8086	Sequence 8086, Ap
38	41.6	3.6	1030	14	US-11-174-751-7	Sequence 7, Appli
39	41.6	3.6	1032	14	US-11-174-751-8	Sequence 8, Appli
40	41.4	3.5	1862	14	US-11-136-527-2377	Sequence 2377, Ap
41	40.2	3.4	3643	14	US-11-136-527-3725	Sequence 3725, Ap
42	40	3.4	1691140	14	US-11-091-018-1	Sequence 1, Appli
43	39.8	3.4	597	6	US-09-925-065A-573093	Sequence 573093,
44	39.8	3.4	1928	14	US-11-136-527-3085	Sequence 3085, Ap
45	39.8	3.4	2260	14	US-11-090-439-15	Sequence 15, Appl

#### ALIGNMENTS

#### RESULT 1

US-11-241-956-19  
; Sequence 19, Application US/11241956  
; Publication No. US20060024792A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;  
; APPLICANT: GRAUL Richard C.; CHAMLA, Narinder K.;  
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;  
; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOULEY, Catherine M.;  
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;  
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;  
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;  
; APPLICANT: YUE, Henry; LU, Yan;  
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;  
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;  
; APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;  
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: PI-0236 USN  
; CURRENT APPLICATION NUMBER: US/11/241.956  
; CURRENT FILING DATE: 2005-10-04  
; PRIOR APPLICATION NUMBER: US/10/398,036  
; PRIOR FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: PCT/US01/30661  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/245,855  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/242,322  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/240,589  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 60/249,343  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/247,587  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/245,900  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/242,223  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: US 60/236,546  
; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PERL Program  
; SEQ ID NO 19  
; LENGTH: 1326  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7474823CB1  
US-11-241-956-19

Query Match 23.1%; Score 270; DB 14; Length 1326;  
Best Local Similarity 76.7%; Pred. No. 5.1e-61;  
Matches 330; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 191 GTGCAATGCAATTCCTCTGTACATCTTCTCGTCACTTCTGCACTTCTGGAAGC 250  
Db 353 GTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTCAATGGGATTTTGAAGG 412  
Qy 251 AAGCTTGATATTTGGCTCAATTAATGACTATCTTTATGTACAGCATCTGTGTATAATA 310  
Db 413 AATCTGTGATATTTGGCTCAATTAATGACTATCTTTATGTACAGCATCTGTGTATAATA 472  
Qy 311 TTGTCCTCATCAGCTACGATCGCTACCAAGTCAGTCTCAAAATGCCGTGTGTATAGAGCTC 370  
Db 473 TTGTCCTCATCAGCTACGATCGATACCTGTTCAGTCTCAAAATGCCGTGTGTATAGAGCTC 532  
Qy 371 AGCACTCGGACCTGGAAATTCGCTACTCAGATGGTGGCTGTTGGATATTCCTCTCA 430  
Db 533 AACATACCTGGGCTCTTGAAGATTTCTTCTGTATGTTGGCGTGTGGGCTTCT 592  
Qy 431 TGACAAATGGGCCGATTCGATTTTCAGACTCTTGCAGAAATAGCACTACAGAAATGTG 490  
Db 593 TAGTGAATGGGCCAATGATTTAGTTTCAGAGTCTTGGAAAGTGAAGTAGTGAATGTG 652  
Qy 491 AACCTGGATTTTAAAAAAGTGTACTTTTGTCTCCCTACATCATATTTGGAATTCCTGA 550  
Db 653 AACCTGGATTTTTCGGAAATGGTATACATCTTGGCAATCATCATCTTCTGGAATTCGTGA 712  
Qy 551 TCCCACTCTGTAGTGTCTTATTTTCAGCGCCCATATTTACTGAGCTGTGGAGCGAG 610  
Db 713 TCCCACTCATCTAGTCGCTTATTTTCAACATGAATATTTTATTTGAGGCTGTGGAGCGGTG 772  
Qy 611 AGAACTGTAG 620  
Db 773 ATCATCTCAG 782

RESULT 2

US-11-036-196-2003  
; Sequence 2003, Application US/11036196  
; Publication No. US20060078900A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgins, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/11/036.196  
; CURRENT FILING DATE: 2005-01-18  
; PRIOR APPLICATION NUMBER: US/10/152.319  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2003  
; LENGTH: 2761  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_053506  
US-11-036-196-2003

Query Match 10.5%; Score 123; DB 11; Length 2761;  
Best Local Similarity 54.0%; Pred. No. 6.3e-22;  
Matches 305; Conservative 0; Mismatches 245; Indels 15; Gaps 2;

Qy 59 TAATGTCTTTACTAGCTATTGCTATATGTTAGGCAATGCTGGTCAATTTTAGCTTTTA 118  
Db 456 TCAATGGCGCTCATCGTGGCCACAGTACTGGGCAAGCGCTGGTCACTGCTCGCCTCG 515  
Qy 119 TTGTGGACAGAAATCTTACATCGAAGTAATTAATCTTTTCTTAACTTGGCCATTCAG 178  
Db 516 TGGCGGATTCAGCGCTCCGCAACAGAACTTCTTCTGCTCAACCTGCCATCTCCG 575  
Qy 179 ACTTCTTTGGGTGCAATTCCTCTGTACATACCTTCTTCTGCTGCTGCTGCTTAC---T 235  
Db 576 ACTTCTCTGGGTGCTTCTGCACTCCCATTTGACGTACCTATGCTGACCGCGCTT 635  
Qy 236 GGAATCTCGAAAGCAAGCTTGTGTTTGGGCTCATTAAGTACTACTTCTTATGTACAG 295  
Db 636 GGAATCTCGCGCGGCGCTCTGCAAGCTGTGGTGGTAGACTACTACTTGTGCTT 695  
Qy 296 CATCTGTGTAATAATTTGCTCTCATCAGCTACGATCGTACCAAGTCAAGTCTCAAAATGCCG 355  
Db 696 CTTGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTCAGTCACTCGAGCTG 755  
Qy 356 TGTGGTATAGAGCTCAGACTCTGGCACTGGGAAATTTGCTACTCAGATGGTGGCTGTTT 415  
Db 756 TCTCTACAGGGCCAGCAGGGGACACAGACGCGGCGTTTCGGAAGATGGCACTGGTGT 815  
Qy 416 GGAATTTCTCTCATGACAAATGGGCGCATGATTTCTGATTTTCTGAGCTCTTGGCAGAATA 475  
Db 816 GGGTGTGGCTTCTCTGCTGTATGGGCTGCCATTCCTGAGTTGGAGTACTCTGTCTGGTG 875  
Qy 476 GCACTACAG-----AATGTGAACCTGGAATTTTAAAGTGGTACTTTGCTC 523  
Db 876 GCAGTTCCATCCCGAGGGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCA 935  
Qy 524 TCCCTACATCATTTATTTGGAATTCCTGATCCCATCTTGTAGTCTTATTTAGCGGCC 583  
Db 936 TCAGGGCTCCACCCCTCGAGTTCTTTCACGGCCCTTCTCCTCAGCGTTTACTCTTCAACCTCA 995  
Qy 584 ATATTTACTGGAGCTGTGGAAGCG 608  
Db 996 GCATCTACTGAACATCCAGAGGGG 1020

RESULT 3

US-11-136-527-3990  
; Sequence 3990, Application US/11136527  
; Publication No. US2005028750A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M







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; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14

Query Match      6.1%; Score 71.2; DB 14; Length 1974;
Best Local Similarity 53.6%; Pred. No. 2.8e-08;
Matches 173; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 53 CATTTTTAATGCTCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTGCTCAATTTTAG 112
Db 215 CTTTCTTAACGGGCATCTGCGCTTGTGACCATCATCGGCAACATCTGGTAATTTGT 274

Qy 113 CTTTATTGTCGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCA 172
Db 275 CATTTAAGGTCAACAAGCAGCTGAAGAGCGGTCAACAACACTACTTCTCTTAAGCCTGGCCT 334

Qy 173 TTGCAGACTTCTTTGTCGGTGCATTTGCAATTCCTCTGTACATACCTTCTCTGCGC---TGA 229
Db 335 GTGCCGATCTGATTTATCGGGTCAATTTCAATGAATCTGTTTACGACCTTACATCATCA 394

Qy 230 CTTTACTGCATCTTCGGAAGCAAGCTGTGTAATTTTGGCTCATTAACGACTATCTTTAT 289
Db 395 ATCGATGGGCTTAGGGAACCTTGGCCTGTGTGACCTCTGCTGCGCATTAACGACTATGAGCCA 454

Qy 290 GTACAGCATCTGTCTATAATATTTCTCTCATCAGTACGATCGCTACAGTCACTCTCAA 349
Db 455 GCATGCTCTGTTATGATCTCTGCTCATCAGCTTGACAGATCACTTTTCCATCAGCA 514

Qy 350 ATGCCGCTGTGTATAGACTGCTGAC 373
Db 515 GGCCTGCTCACGTACCGAGCAAC 538

RESULT 9
US-11-136-527-3691
; Sequence 3691, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3691

Query Match      6.1%; Score 71; DB 14; Length 2348;
Best Local Similarity 53.6%; Pred. No. 3.5e-08;
Matches 171; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 53 CATTTTTAATGCTCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTGCTCAATTTTAG 112
Db 343 CTTTCTTAACGGGCTTCTGTCATTTGGTACCATCATTTGGCAACATCTTTGTCAATTTGG 402

Qy 113 CTTTATTGTCGACAGAAATCTTAGACATCGAAGTAATTAATTTTCTTAACCTGGCCA 172
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Db 403 CCTTCAAGGTCAACAAACAGCTGAAGACAGTCAACAACTACTTCTCTTAAGCCTGGCCT 462
Qy 173 TTGCAGACTTCTTTGTCGGTGCATTTGCAATTCCTCTGTACATACCTTCTGCTGCTGACTT 232
Db 463 GTGCAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACTACCTACATCATATGA 522
Qy 233 AC---TGGACTTCTGGAAGCAAGCTGTGTAATTTTGGCTCATTAACGACTATCTTTAT 289
Db 523 ACCGTTGGGCACTGGGGAACCTTAGCCTGGGACCTCTGCTCTCCATTAATGATGTGGCA 582
Qy 290 GTACAGCATCTGTCTATAATATTTCTCTCATCAGTACGATCGCTACAGTCACTCTCAA 349
Db 583 GCAATGCTCTGTCTCATGATCTGCTGCTCATCAGCTTGACAGGTACTTTTCCATCACTA 642
Qy 350 ATGCCGCTGTGTATAGACTGCTGAC 368
Db 643 GGCCACTCACCTACCGAGC 661

RESULT 10
US-11-036-196-1495
; Sequence 1495, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3578
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_012527
US-11-036-196-1495

Query Match      6.1%; Score 71; DB 11; Length 3578;
Best Local Similarity 53.6%; Pred. No. 4.2e-08;
Matches 171; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 53 CATTTTTAATGCTCTTTACTAGCTATTGCTATAATGTTAGGCAATGCTGCTGCTCAATTTTAG 112
Db 252 CCTTCTTAACGCTTCTGTCATTTGGTGGACCATCATTTGGCAACATCTTTGTCAATTTGG 311
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Qy 113 CTTTATTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACTTGGCCA 172
Db 312 CTTTCAAGGTCAACAACAGCTGAAGACAGTCAACACTACTTCTCTTAAGCTGGCCT 371
Qy 173 TTGCAGACTCTTTGTGGGTGCAATGGAATTCCTCTGTACACACCTTCCTCGCTGACTT 232
Db 372 GTGCAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACTACCTACATCATTA 431
Qy 233 AC---TGAAGCTTCGGAACGACCTGTGTATTTTGGCTCATTAATCACTGATCTTTTAT 289
Db 432 ACCGTTGGGCACTGGGGAACCTTAGCCTGGCACTCTGGCTCTCCATTTGACTATGGCCA 491
Qy 290 GTACAGCATCTGTGTATAATATTCTCTCATCAGCTACGATCGCTACCACTGACTCTCAA 349
Db 492 GCAATGCTCTGTCAATGAATCTGTGTCTCATCAGCTTTGACAGTACTTTTCCATCACTA 551
Qy 350 ATGCCGTTGGTATAGAGC 368
Db 552 GGCCACTCACTACCGAGC 570

RESULT 11
US-11-136-527-2030
; Sequence 2030, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2030
; LENGTH: 4095
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2030

Query Match 6.1%; Score 71; DB 14; Length 4095;
Best Local Similarity 53.6%; Pred. No. 4.5e-08;
Matches 171; Conservative 0; Mismatches 145; Indels 3; Gaps 1;
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Qy 53 CATTTTAAATGTCTTTACTAGCTATTCGTATAATGTTAGGCAATGTCGTGTCATTTTAG 112
Db 759 CTTCTTAAACVGGCTTCTCGCATTTGGTGACCATCAATGGCAACATCCTTGTCAATGG 818
Qy 113 CTTTATTGTGGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACTTGGCCA 172
Db 819 CTTTCAAGGTCAACAACAGCTGAAGACAGTCAACAACACTCTCCTCTTAAGCCTGGCCT 878
Qy 173 TTGCAGACTCTTTGTGGGTGCAATTCCTCTGTATACATACCTTCTCTCGCTGACTT 232
Db 879 GTGCAGACCTGATCATCGGGGTCAATTCATGAACCTGTTCACTACCTACATCATTA 938
Qy 233 AC---TGAAGCTTCGGAACGACCTTTGTGTATTTTGGCTCATTAATCACTGATCTTTAT 289
Db 939 ACCGTTGGGCACTGGGGAACCTTAGCCTGGCACTCTGGCTCTCCATTTGACTATGGCCA 998
Qy 290 GTACAGCATCTGTGTATAATATTCTCTCATCAGCTACGATCGCTACCACTGACTCTCAA 349
Db 999 GCAATGCTCTGTCAATGAATCTGTGTCTCATCAGCTTTGACAGTACTTTTCCATCACTA 1058
Qy 350 ATGCCGTTGGTATAGAGC 368
Db 1059 GGCCACTCACTACCGAGC 1077
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RESULT 12
US-11-127-877-4
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; Sequence 4, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-4

Query Match 5.9%; Score 69.4; DB 14; Length 1401;
Best Local Similarity 52.2%; Pred. No. 7.3e-08;
Matches 204; Conservative 0; Mismatches 181; Indels 6; Gaps 2;

Qy 70 CTAGCTATTCTATATAGTTAGGCAATGTCGTGTCATTTTAGCTTTTATTGTCGACAGA 129
Db 97 CTCAGTTTGTGTGACCATTTATCGGGAACATCTTAGTCTATGTTTCCATTAAAGTCAACGC 156
Qy 130 AATCTTAGACATCGAAGTAATTAATTTTCTTAACTTGGCCATTGAGACTTCTTTGTG 189
Db 157 CACCTCAGACCGTCAACAATTAATTTTATCAGCTTGGCTGTGCTGACCTTATCATTA 216
Qy 190 GGTGCAATTCGAATTCCTCTGTATACATACCTTCTCTCGCTGAC---TTACTGGACTTCTGGA 246
Db 217 GGTGTTTCTCCATGAACCTTGACACCTCTACACTGTGATGTTGTTTACCTGCTTGGGA 276
Qy 247 AAGCAAGCTTGTGTATTTTGGCTCATTAATGCTGATCTTTTATGTACAGCATCTGTGTAT 306
Db 277 CCTGTGTGTGTGACCTTTTGGCTAGCCCTGAGCTATGTGCTGACCAATGCTCTCAGTTATG 336
Qy 307 AATATTCTCTCATCAGTACGATCGCTACAGTCACTCTCAAAATGCCGTGTGTATAGA 366
Db 337 AATCTGCTCATCATCAGCTTTGACAGTACTTCTGTGTCAAAAACCTCTGACCTACCCA 396
Qy 367 GCTCAGCACTCTGGCACCTCGAAAAATTTGCTACTCAGATGGTGGCTGTTTGGATATTTCTCC 426
Db 397 GTCAGGGGAC---CACAAAATGGCAGGTATGATGATTGCAGCTGCTGGTCTCTCTCT 453
Qy 427 TTCAATGCAAAATGGCGGATGATTTCTGATTT 457
Db 454 TTCATCTCTCTGGGCTCCAGCCATTCTCTCT 484

RESULT 13
US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2435
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; LENGTH: 2733  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2435

Query Match 5.8%; Score 68.4; DB 14; Length 2733;  
Best Local Similarity 52.4%; Pred. No. 1.8e-07;  
Matches 175; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 43 ATTCTTTGACATTTTAAATGCTTTACTAGCTATTGCTATTAATGTTAGGCAATGCTGTG 102  
Db 1061 ATTACTATTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120  
Qy 103 GTCATTTTAGCTTTTATTGTCGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTT 162  
Db 1121 GTCATGATCTCTTCAAAAGTCAACAGTCAGCTCAAGACAGTTAACTACTACCTGCTC 1180  
Qy 163 AACTTGGCCATTCGACAGCTTCTTTGCTGGTGAATTTGCAATTCCTCTCTACATACCTTCC 222  
Db 1181 AGCTTGGCTGTGACAGCTCATCATTTGGCATCTTCTCCATGAACTCTACAGACCTAC 1240  
Qy 223 TCGCTGACTTA---CTGACCTTCTGGAAGCAAGCTTGTATTTTGGCTCAATTAAGTAC 279  
Db 1241 ATCTCTATGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300  
Qy 280 TATCTTTTATGTACAGCATCTGTGTATTAATTTGCTTCATCAGCTACGATCGCTACCG 339  
Db 1301 TATGTAGCCAGCAATGCTTCTGTATGAACCTTCTGGTGAATAGTTTGTGCTGCTACTTT 1360  
Qy 340 TCAGTCTCAAAATCGCTGTGTATATAGACTCAGC 373  
Db 1361 TCCATCACAGACCACTGACGTACCGGCCAAGC 1394

## RESULT 14

US-11-127-877-5  
; Sequence 5, Application US/11127877  
; Publication No. US2005028756SAI  
; GENERAL INFORMATION:  
; APPLICANT: Merckhiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad P. P.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-5

Query Match 5.5%; Score 63.8; DB 14; Length 2699;  
Best Local Similarity 51.3%; Pred. No. 3e-06;  
Matches 174; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

Qy 43 ATTCTTTGACATTTTAAATGCTTTACTAGCTATTGCTATTAATGTTAGGCAATGCTGTG 102  
Db 405 ATCACCATTGACGTGTGACTGTGTGTAGCTGATCACCATTGTGGCAATGCTGTG 464  
Qy 103 GTCATTTTGTAGCTTTTATTGTCGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTT 162  
Db 465 GTCATGATCTCTTCAAGTCAACAGCCAGCTCAGACAGTTACACTATTAATCTGCTC 524  
Qy 163 AACTTGGCCATTGACAGACTTCTTTTGGTGGTGAATTTGCAATTCCTCTGTATACACTTCC 222

Db 525 AGCTTAGCTGTGACAGATCTCATATTGGAATCTTCTCCATGAACCTCTACACCCTAC 584  
Qy 223 TCGCTGACTTA---CTGACCTTCTGGAAGCAAGCTTGTGTATTTTGGCTCAATTAAGTAC 279  
Db 585 ATCTCTATGGAAGCTGCTGCTCTCGGAGTCTGGCTTGTGACCTTTGGCTTGCACCTGGAC 644  
Qy 280 TATCTTTTATGTACAGCATCTGTGTATTAATTTGCTTCATCAGCTACGATCGCTACCG 339  
Db 645 TACGTGGCCAGCAACGCTTCTGTATGAACCTTCTGGTGAATCAGTTTGTGACCGTACTTT 704  
Qy 340 TCAGTCTCAAAATCGCTGTGTATATAGACTCAGCACTCT 378  
Db 705 TCCATCACAGACCTTGCATATTCGGGCCAAGCGTACT 743

## RESULT 15

US-11-136-527-751  
; Sequence 751, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; PRIOR FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 751  
; LENGTH: 3741  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-751

Query Match 4.6%; Score 53.8; DB 14; Length 3741;  
Best Local Similarity 47.5%; Pred. No. 0.0016;  
Matches 161; Conservative 9; Mismatches 166; Indels 3; Gaps 1;

Qy 93 CAATGTGCTGTCTCATTTTATGCTTTTATTTGTGACAGAAATCTTAGACATCGAAGTAATTA 152  
Db 1122 CAACCTGTGTGTGTGTATGCGTGTGCRCAAGTGAAGCAAGCTACACCGTGGGCACT 1181  
Qy 153 CTTTTTTTCTTAACCTGGCCATTCAGACTTCTTTTGTGGGTGCAATTCGAATTCCTCTGTA 212  
Db 1182 RTACATTTGTCAGCTGCTGCTGTCGTCAGACCTGATTTGTAGGGCAGTGTGTCATGCCCATGAA 1241  
Qy 213 CATAC---CTTCTCGCTGACTTACTGACCTTCTGGAAGCAAGCTTGTGTATTTTGGCT 269  
Db 1242 CATCTCTATCTATCATGACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301  
Qy 270 CATTACTGACTATCTTTTATGTACAGCATCTGTGTATTAATTTGTCCTCATCAGCTACGA 329  
Db 1302 YTCTATGATTTATGTGGCCAGCAGCATCATCTTTAGTGTCTTCATCTCTGTGTATTTGA 1361  
Qy 330 TCGCTACCACTGACTCTCAAAATGCGGTGTGTATAGAGCTCAGCACTCTGGCACTCGGAA 389  
Db 1362 TCGCTACCGCTCTGTCAGCAACCCCTCCGGTACTGAGGTAYCGAACCAAGACCCGKGC 1421  
Qy 390 AATTGCTACTCAGATGGTGGCTGTGTGATTAATTCCTTT 428  
Db 1422 TTCMGCTACCATCTCGGGGCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1460

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Job time : 628 secs

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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:43:21 ; Search time 46 Seconds  
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699.149 Million cell updates/sec

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Perfect score: 2036  
Sequence: 1 MLANNSTIALTSIKISLTLFL.....LKILPVRQSTPPHNRISIST 389

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/iaa/6\_COMB.pep.\*  
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6: /cgn2\_6/prodata/1/iaa/baCkfilea1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1308.5	64.3	390	2	US-09-414-010-2
2	1308.5	64.3	390	2	US-09-812-216-2
3	1308.5	64.3	390	2	US-09-875-076-14
4	694.5	34.1	413	2	US-09-891-053-1
5	689.5	33.9	445	1	US-08-985-090-2
6	689.5	33.9	445	2	US-09-165-543-2
7	689.5	33.9	445	2	US-09-167-354-7
8	689.5	33.9	445	2	US-09-642-855-7
9	689.5	33.9	445	2	US-09-642-514-7
10	689.5	33.9	445	2	US-09-642-852-7
11	689.5	33.9	445	2	US-10-453-106-1
12	689.5	33.9	449	2	US-09-949-016-10930
13	689.5	33.9	453	2	US-09-891-053-20
14	688.5	33.8	445	2	US-10-453-106-2
15	681.5	33.5	445	2	US-09-165-543-5
16	681.5	33.5	445	2	US-09-891-053-25
17	681.5	33.5	445	2	US-10-453-106-3
18	609.5	29.9	351	2	US-09-524-162-2
19	546	26.8	362	1	US-08-985-090-5
20	546	26.8	362	2	US-09-165-543-32
21	412	20.2	355	1	US-08-118-270-11
22	412	20.2	355	4	PCT-US93-08528-11
23	410.5	20.2	348	1	US-08-118-270-13
24	410.5	20.2	348	4	PCT-US93-08528-13
25	403.5	19.8	590	2	US-09-538-092-967
26	398.5	19.6	590	2	US-09-826-509-517
27	390.5	19.2	532	2	US-09-826-509-521

28	388.5	19.1	479	1	US-08-313-553-7	Sequence 7, Appli
29	388.5	19.1	479	2	US-08-767-993-7	Sequence 7, Appli
30	385.5	18.9	429	1	US-08-748-485-7	Sequence 7, Appli
31	385.5	18.9	429	2	US-09-919-039-6	Sequence 6, Appli
32	385.5	18.9	466	1	US-08-722-001-12	Sequence 12, Appli
33	385.5	18.9	466	1	US-08-467-568-11	Sequence 11, Appli
34	385.5	18.9	466	1	US-09-030-582-11	Sequence 11, Appli
35	384.5	18.9	460	2	US-09-826-509-513	Sequence 513, App
36	384.5	18.9	466	1	US-08-406-855A-23	Sequence 23, Appl
37	384.5	18.9	466	2	US-09-206-899-23	Sequence 23, Appl
38	384.5	18.9	466	2	US-09-688-415-11	Sequence 11, Appl
39	384	18.9	466	1	US-08-334-698-6	Sequence 6, Appli
40	384	18.9	466	1	US-08-228-932-6	Sequence 6, Appli
41	384	18.9	466	1	US-08-468-933-6	Sequence 6, Appli
42	384	18.9	466	1	US-08-722-001-28	Sequence 28, Appl
43	384	18.9	466	1	US-08-406-855A-6	Sequence 6, Appli
44	384	18.9	466	1	US-08-722-190-6	Sequence 6, Appli
45	384	18.9	466	2	US-08-244-354-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-414-010-2  
; Sequence 2, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas W.  
; APPLICANT: Monson, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; APPLICANT: Wang, Suke  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-414-010-2

Query Match	64.3%	Score 1308.5;	DB 2;	Length 390;
Best Local Similarity	65.1%;	Pred. No. 3.1e-103;		
Matches 252;	Conservative 48;	Mismatches 84;	Indels 3;	Gaps 3;
QY	5	NSTIALT-SIKISLTFMLSLAIAIMGNVVVILAFIVDRNLRHSNYPFLNLAIADPFFV 63		
Db	5	NSTINLSLSTRVTLLAFNLSLVAFLMGNVALVILAFVVDKNLRHSNYPFLNLAIADPFFV 64		
QY	64	GAIAIPLYPSSLTYTSTGKQACFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVWYRA 123		
Db	65	GVISPLIPIHTLPEDWFGKEICFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVWYRA 124		
QY	124	QHSQGWKIATQWAVWIFPMTNGPMILISQWQNTTECEPGFLKKNYFALPTSLLPFL 183		
Db	125	QHTGLVKITVLMVAVWVLAFLVNGPMILVSRWQDEGSECEPGFSEWYLAITSFLEPV 184		
QY	184	IPILAVYFSAHYWLSMKREKLSCLGHPVLPSDSSSDHGHSCQDQDSRATIPARKE 243		
Db	185	IPVILVAFVNMNIVWSLWKRDHLSRQSHPGJLTA-VSSNICGHSFRGSRSSRSASSTE 243		
QY	244	TTASIGSDKSRKSLPISIRAYKNSNVIASQWGLSHSDSLAQQRHIEIFRARKLAK 303		
Db	244	VPASPHSERQKSLMFSSTRTKNSNTIASQWGSQSDSVALHQREHVELLRARLAK 303		
QY	304	SLAIIILAAPAICWAPYSLTWIVYSPFRNLTKSTWYHTAFWLQWNSFVNPFLPLCHK 363		





Db 185 IPVLVAYNNIYWSLWDRDLHSCQSHPGITA-VSSNICGSHFAGRLSSRRSLASST 243  
QY 244 TTASLGSDKRRKSLPSIRAYKNSNVIAASKGFLSHSDSLAQOREHIELFRARKLAK 303  
Db 244 VPASPHSERQRKSLSPSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRARLAK 303  
QY 304 SLAIIILAPAIWAPYSLTIVYSPPPERNLTKSTWHTAFWLOWNSFVNPFLPLCHK 363  
Db 304 SLAIIILGVAVCWAPYSLTIVYSPSSATGPKSVWYRIAFWLOWNSFVNPFLPLCHK 363  
QY 364 RFQKAPLKILPVRRSTP-PHNRISIT 389  
Db 364 RFQKAPLKILFCIKKQPLPSQHSRVS 390

## RESULT 4

US-09-891-053-1  
; Sequence 1, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-891-053-1

Query Match 34.1%; Score 694.5; DB 2; Length 413;  
Best Local Similarity 39.2%; Pred. No. 5.1e-51;  
Matches 159; Conservative 66; Mismatches 130; Indels 51; Gaps 12;  
QY 3 ANNSTIALTSIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSNVFFLNLAIDPF 62  
Db 26 ARGSAANTAV---LAALMALIVATVIGNALVMAFVADSLRTQNNFFLNLAISDFL 82  
QY 63 VGAIAPILYIPSSLT-YMTSGKQACVFWLITDYLCTASVNVNIVLISYDRYOSVSNVWY 121  
Db 83 VGAFICPLVVPVLTGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSY 142  
QY 122 RAQHSQTKIATQWAVWIFSPWNGPMLIISDSQW-----NSTTE--CEPGFLKKWYPA 174  
Db 143 RAQQGDTRRAVRKMLVWVLAFLYGPAIL---SWEYLSGGSSSIEGHCYAEFFYNWYPL 199  
QY 175 LPTSLEFLIPLLVAYFSAHYWLSWKREKL---SRCLSHPLVPSDSSS-----222  
Db 200 ITASTLEFPTPLSVTFNLSIYLNIOQRTRULRGREAGPEPPDQAQSPPPAPPSCW 259  
QY 223 -----DHGHSCKQDPDSRATLPARKETASLGSKSRKSSLLPSIRAYKNSNVIAKMG 277  
Db 260 GCWPKHGEA-----MPLHSGSSSRCTERPR---SLKRGSKPSASSASLEKRMK 306  
QY 278 FLSHSDSLAQOREHIELFRARKLAKSLAIIILAPAIWAPYSLTIVYSPPPERNLTKS 337

Db 307 MVSQS-----ITQR--FRLSRDKKVAKSLAIIVSIFCLCWAPYTLMLIRAAHGRCI-PD 359  
QY 338 TWYHTAFWLOWNSFVNPFLYPLCHKRFQKAFKILPVRRQSTPPH 383  
Db 360 WYETSFLLWANSVNPVLYPLCHYSFRAFTKLLCPQKLVQPH 405  
RESULT 5  
US-08-985-090-2  
; Sequence 2, Application US/08985090  
; Patent No. 5885893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D. J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,090  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jean M. Silveri  
; REGISTRATION NUMBER: 39,030  
; REFERENCE/DOCKET NUMBER: MNI-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-985-090-2

Query Match 33.9%; Score 689.5; DB 1; Length 445;  
Best Local Similarity 37.3%; Pred. No. 1.5e-50;  
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;  
QY 3 ANNSTIALTSIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSNVFFLNLAIDPF 62  
Db 26 ARGSAANTAV---LAALMALIVATVIGNALVMAFVADSLRTQNNFFLNLAISDFL 82  
QY 63 VGAIAPILYIPSSLT-YMTSGKQACVFWLITDYLCTASVNVNIVLISYDRYOSVSNVWY 121  
Db 83 VGAFICPLVVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSY 142  
QY 122 RAQHSQTKIATQWAVWIFSPWNGPMLIISDSQW-----NSTTE--CEPGFLKKWYPA 174  
Db 143 RAQQGDTRRAVRKMLVWVLAFLYGPAIL---SWEYLSGGSSSIEGHCYAEFFYNWYPL 199  
QY 175 LPTSLEFLIPLLVAYFSAHYWLSWKREKL---SRCLSHPLVPSDSSS-----222  
Db 200 ITASTLEFPTPLSVTFNLSIYLNIOQRTRULRGREAGPEPPDQAQSPPPAPPSCW 259  
QY 223 -----DHGHSCKQDPDSR-----ATL-----PARKETTASLGSKD 252  
Db 260 GCWPKHGEAM---PLHRYGVGEAAVGAAGENTLGGGGGGSVASPTSSSGSSSRGT 316  
QY 253 SRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAKSLAIIILAP 312

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Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSFT-----QRFSLGRDRKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPLYPLCHKRFOKAFUKI 372
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLIKIQPHS 438

RESULT 6
US-09-165-543-2
; Sequence 2, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-2

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFMLSLAIATMLGNVVVILAFVDRNLHRHSNYFFLNLAIDFF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVGLGNALVLAFAVDSSLRQTQNNFFLNLAISDFL 82
QY 63 VGAIAPIYIPSSLT-YWTSKQACVFLLITDYLCTASVNVILISYDRYQSVNAVWY 121
Db 83 VGAFCIPLYVPVLTGRWTFGRGLCKLWLVDDYLLCTSSAFNVLISYDRFLSVTRAVSY 142
QY 122 RAQHSQGTWKIATQMVAVWIFSMFMTNGPMLISDSWQ-----NSTTE--CEPGFLKKWYFA 174
Db 143 RAQQQDTRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFL 199
QY 175 LPTSLLLEFLIPILLVAYPSAHYWSLWKREKL-----SRCLSHVPLPSDSSSS----- 222
Db 200 ITASTLEFFTPLSVTFNLSIYLNIQRRTRLRDGAREAGPEPPPPGCGW 259
QY 223 ----DHGHSCKQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSFT-----QRFSLGRDRKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPLYPLCHKRFOKAFUKI 372
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFRRAFTKL 426
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QY 223 ----DHGHSCKQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSFT-----QRFSLGRDRKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPLYPLCHKRFOKAFUKI 372
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFRRAFTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLIKIQPHS 438

RESULT 7
US-09-167-354-7
; Sequence 7, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Javashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-167-354-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFMLSLAIATMLGNVVVILAFVDRNLHRHSNYFFLNLAIDFF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVGLGNALVLAFAVDSSLRQTQNNFFLNLAISDFL 82
QY 63 VGAIAPIYIPSSLT-YWTSKQACVFLLITDYLCTASVNVILISYDRYQSVNAVWY 121
Db 83 VGAFCIPLYVPVLTGRWTFGRGLCKLWLVDDYLLCTSSAFNVLISYDRFLSVTRAVSY 142
QY 122 RAQHSQGTWKIATQMVAVWIFSMFMTNGPMLISDSWQ-----NSTTE--CEPGFLKKWYFA 174
Db 143 RAQQQDTRAVRKMLLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFL 199
QY 175 LPTSLLLEFLIPILLVAYPSAHYWSLWKREKL-----SRCLSHVPLPSDSSSS----- 222
Db 200 ITASTLEFFTPLSVTFNLSIYLNIQRRTRLRDGAREAGPEPPPPGCGW 259
QY 223 ----DHGHSCKQPPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIASKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPSASSASLEKRMKMWVSQSFT-----QRFSLGRDRKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFFPERNLTKSTWHTAFWLOWFNSFVNPLYPLCHKRFOKAFUKI 372
Db 368 GLCWAPYTLMIIRAAC-HGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFRRAFTKL 426
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QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLKIQPHS 438

RESULT 8
US-09-642-855-7
; Sequence 7, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: ORT1290
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-642-855-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFLMSLAIAMLGNNVVILAFIVDRNLHRSNYFFNLAIADPF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVLGNALVMLAFVADSLRTQNNFFNLAIADPF 82
QY 63 VGAIAPLYIPSSLT-YWTSGKQACVFWLITDYLLCTASVNVILISYDRVQSNSNAVY 121
Db 83 VGAFICPLYVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVILISYDRFLSVTRAVSY 142
QY 122 RAQSGTWKIAQMVAVNIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174
Db 143 RAQQDTRRAVRKMLLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFL 199
QY 175 LPTSLEFLIPIILLVAYPSAHYNSLWREKL-----SRCLSHVLPSSSSS----- 222
Db 200 ITASTLEFPPLSVTFNFNLSIYLNQIRTRLRLDGAREAAAGPEPPPEAQPSPPPPGCW 259
QY 223 -----DHGHSCEQDPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPASASSASLEKRMKMWVSQSFT-----QRFLSDRDKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWFNFSVNPFLYPLCHKRFOKAFKI 372
Db 368 GLCWAPYTLMLIIRAC-HGHCVDPDYWYETSPWLLWANSVNPVLYPLCHHSFRAPTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLKIQPHS 438

RESULT 9
US-09-642-514-7
; Sequence 7, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JWV
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-642-855-7

Query Match 33.9%; Score 689.5; DB 2; Length 445;
Best Local Similarity 37.3%; Pred. No. 1.5e-50;
Matches 161; Conservative 70; Mismatches 132; Indels 69; Gaps 13;

QY 3 ANNSTIALTSIKISLTFLMSLAIAMLGNNVVILAFIVDRNLHRSNYFFNLAIADPF 62
Db 26 ARGFSAAWTAV---LAALMALLIVATVLGNALVMLAFVADSLRTQNNFFNLAIADPF 82
QY 63 VGAIAPLYIPSSLT-YWTSGKQACVFWLITDYLLCTASVNVILISYDRVQSNSNAVY 121
Db 83 VGAFICPLYVPVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVILISYDRFLSVTRAVSY 142
QY 122 RAQSGTWKIAQMVAVNIFSPMTNGPMILISDSWQ-----NSTTE--CEPGFLKKWYPA 174
Db 143 RAQQDTRRAVRKMLLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFL 199
QY 175 LPTSLEFLIPIILLVAYPSAHYNSLWREKL-----SRCLSHVLPSSSSS----- 222
Db 200 ITASTLEFPPLSVTFNFNLSIYLNQIRTRLRLDGAREAAAGPEPPPEAQPSPPPPGCW 259
QY 223 -----DHGHSCEQDPDSR-----ATL-----PARKETTASLGSDK 252
Db 260 GCWQKGHEAM---PLHRYGVGEAAVGAAGATLGGGGGGSVASPTSSSGSSSRGTER 316
QY 253 SRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAKSLAILLAAP 312
Db 317 PR---SLKRGSKPASASSASLEKRMKMWVSQSFT-----QRFLSDRDKVAKSLAVIVSIF 367
QY 313 AICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQWFNFSVNPFLYPLCHKRFOKAFKI 372
Db 368 GLCWAPYTLMLIIRAC-HGHCVDPDYWYETSPWLLWANSVNPVLYPLCHHSFRAPTKL 426
QY 373 LPVRRQSTPPHN 384
Db 427 LCPQKLKIQPHS 438

RESULT 10
US-09-642-852-7
; Sequence 7, Application US/09642852
; Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JWV
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
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87	VGAFCIPIYVPVYL	TGRWTFGRGLCKMLWVDYLLCTSSAFNVILISDRFLSVTRAVSY	146
122	RAQHSWTGKIATQ	MAVAVWIFSFMTNGPMLISDSWQ-----NSTYTE--CEPGFLKKWTFA	174
147	RAOQGDTRBARVK	MLLVWVLAFLLYGPAIL---SWEYLSGGSSIEPEGHYAEEFFYNWYFL	203
175	LPTSLEPLIPI	LLVAVYPSAHHYNSLWTKREKL-----SRCLSHVLPDSOSSS-----	222
204	ITASTLEFPTPL	SVTFFNLSTYLIQRRTRLRLDGAAREAGPEPPEAQSPPPPPGCV	263
223	-----DIGHSC	ROQDPDSR-----ATL-----PARKETTASIGSDK	252
264	GCWOKGHGRAM	---PLHHYGVGEAAVGAAGEATLGGGGGGGSVASPTSSSGSSSRGRTE	320
253	SRRKSSLLPS	TRAVKNSNVIAASKMGFLGSHSDLSALQORHEHTLPARKLAKSLAILLAAF	312
321	PR---	SLKRGSKPNSASSASLEKRWKWSQSFT-----QRFELSDRDKVAKSLAVISIF	371
313	AICWAPYSLAT	TVIYSFFPERNLTKSTWYHTHFAWLOWFNSVFNPFYPLCHRFKQAFUKI	372
372	GLCWAPYTLMI	IRAAC-HGHCVDPWYETSPWLLWANSVNVNPLYPLCHSFRFAFTKL	430
373	LPVRRQSTPP	PN 384	
431	LCPOKLIKIQHS	442	

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RESULT 13
US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takamura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JF99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JF98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-053-20

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	Query Match	33.9%	Score 689.5;	DB 2;	Length 453;
	Best Local Similarity	37.3%	Pred. No. 1.5e-50;		
	Matches 161;	Conservative 70;	Mismatches 132;	Indels 69;	Gaps 13
Qy	3	ANNSTIALTSIKISITFLMSLLATAIMLGNVVVILAFIVDRNLRHSNVFFLNLAIADPFF	62		
Db	26	ARGFSAWTAIV--LAAIMALLIVATVIGNALVMLAFVADSLRTRQNNFFLNLALISDPL	82		
Qy	63	VGAIAIPLYIPSSILT-YMTSGKQACFWMLITDYLLCTASVNVILISIDRYQSQSVNAVY	121		
Db	83	VGAFCIPLYVPVYLTCRTWTFEGRLCKLVLVDYLLCTSSAFNVILISIDRFLSVTRAVSY	142		
Qy	122	RAQHS GTWKIATQVAVVIFSMTNGPMILISDSWQ-----NSTTTE--CEEGFLKKWYFA	174		
Db	143	RAOOGDTRRAVRKMLLVVLAFLYLGPAIL---SWEYLSGGASSIPEGHCYAEFFNNYVFL	199		

Qy	175	LPTSLLEFLPILLVAYFSAHIYWSLWKREKL-----SRCLSHPVLPSSDSSS-----	222
Db	200	ITASTLEFFPFLSVTFNLSIYLNIOQRTRLRLDGAREAAAGPEPPPAQSPPPPPGCM	259
Qy	223	-----DRGHSRCRQDPDSR-----ATL-----PARKETTASLGSOK	252
Db	260	GCWQKGHEAM---PLHRYGVGEAAVGAEGEATLGGGGGGSVASPTSSSGSSSRGTGR	316
Qy	253	SRKSSLLPSIRAYKNQNVITASKMGFLSHSDSLAQOREHTELPRARKLAKSLAILLAAP	312
Db	317	PR---SLKRGSKPSSASGLEKRWKMQSQST-----QRFLSRDRKVAKSLAVIVSIF	367
Qy	313	AICWAPYSLTTVIVSFPFPERNLTKSTWYHTAFMLQWFENSFNPPLYPLCHKRKFQAFLLKI	372
Db	368	GLCWAPYTLMLIIRAAC-HGHCVDPDYVYETSFMLLWANSANVPVLYPLCHHSFRRAFTKL	426
Qy	373	LPVRRQSTPPPHN	384
Db	427	LCPOKLKIOPHS	438

RESULT 14

US-10-453-106-2

Sequence 2, Application US/10453106

Patent No. 6906060

GENERAL INFORMATION:

APPLICANT: Peschke, Bernd

APPLICANT: Hohlweg, Rolf

TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO[1,2-A]PYRAZINES,

TITLE OF INVENTION: OCTAHYDROPIRDO[1,2-A]PYRAZINES AND

TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES

FILE REFERENCE: 6483.200-US

CURRENT APPLICATION NUMBER: US/10/453.106

CURRENT FILING DATE: 2003-06-03

PRIOR APPLICATION NUMBER: US 60/387,047

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 445

TYPE: PRT

ORGANISM: Monkey

US-10-453-106-2

Query Match	33.8%;	Score	688.5;	DB 2;	Length	445;			
Best Local Similarity	37.8%;	pred. No.	1.8e-50;						
Matches	161;	Conservative	66;	Mismatches	142;	Indels	57;	Gaps	12

  

Qy	3	ANNSTIALTSIKISLTFMISLLAIAIMLGNVVVILAFIVDRNLRHRSNYFFLNLAIADPF	62
Db	26	ARGFSAAWTAV--LAALMALLIVATVLGNALVMLAFVADSSLRQTNNFFLNLAIASDFL	82
Qy	63	VGAIAIPLIYTPSSLT-YWTSKQRCQFWLTDYLLCTASVNVILISVDRYQSVSNVAVY	121
Db	83	VGAFCIPLIYPYVLTGRWTTGRLGCKLWLVVDYLLCTSSAFNVLISVDRFLSVTRAVSY	142
Qy	122	RAQSGGTWKIATQMAVYIFSEMTNGPMILISDSQO-----NSTTE--CEPGFLKKWFA	174
Db	143	RAQGNTRAVRKMLLVNVIAFLYLGPAIL---SWEYLSGGSSIPEGHCYAEFFNNWIFL	199
Qy	175	LPSTLSLEFLIPLIVAVFSAHYWSLWKREKL-----SRCLSHPVLPSPDSSSS-----	222
Db	200	ITASTLEFFPFLSVTFENLSIYLNIQRRFRLDLGAREAGCPBPPEAQSPSPPPGCGW	259
Qy	223	-----DHGHC---RODPDSRATLPARKET-----TASIGSPK--SRRKSS	258
Db	260	GCWQKHGEAMPLHRYGVGEAAAGAEAGETALGGGGGGGSAASPTSSSGSSSRGTERPRS	319
Qy	259	LLPSIRAYKSNVTASKMGFLSHSDSLAQOREHIELFRAKLAKSLAILLAAFAICWAP	318

Db 320 LKRGSKPSASSASLEKRMKMSQSFT-----QRFLSRDRKVAKSLAVIVSIIFGLCWAP 373  
Qy 319 YSLTIVYISFFPERNLTKSTWYHTAFWLOWNSFVNPLYPLCHKRFOKAFKILPVBRQ 378  
Db 374 YTLMIIRAAC-HGHCVPDYETSFVLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKL 432  
Qy 379 STPHN 384  
Db 433 KIOPHS 438  
RESULT 15  
US-09-165-543-5  
; Sequence 5, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165.543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 445 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-165-543-5

Query Match 33.5%; Score 681.5; DB 2; Length 445;  
Best Local Similarity 37.6%; Pred. No. 7.1e-50;  
Matches 162; Conservative 65; Mismatches 135; Indels 69; Gaps 13;  
Qy 3 ANNSTIALTSIKISITFLMSLIAIAIMLGNVVILAFIVDRNLHRSNYFFLNLAIDFF 62  
Db 26 ARGFSAAWTAV---LAALMALLIVATVLGNALVAFVADSSLRQTQNNFFLNLAISDFL 82  
Qy 63 VGAIAPIYIPSSLT-YWTSKQACVFWLIITDYLLCTASVYNVILISYDRYQSVSNVWY 121  
Db 83 VGAFCIPLYVPVLTGRWTFGRGLCKLWLVVDYLLCASSVFNVILISYDRFLSVTRA VSY 142  
Qy 122 RAQHSQGWKIATQMVAVVIFPMTGPMILISDSWQ-----NSTTE--CEPGELKKWYFA 174  
Db 143 RAQGGDTTRAVRKMAVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFL 199  
Qy 175 LPTSLLEFLIPLLVAYSIAHYNSLWKREKL---SRCLSHFVLPFSDSSS----- 222  
Db 200 ITASTLEFFTFPLSVTFNFNLSIYLNIQRRTRLRDGGREAGPEPPDAPSPPPAPPCSW 259

Qy 223 -----DHGHSRCQDPDSR-----ATLPARKETTASLGSDK 252  
Db 260 GCWPKGHGEAM---PLHRYGVGEAGPGVEAGEAALGGSGGGAASPTSSSSSSSRGTER 316  
Qy 253 SRRKSSLLPSIRAYKNSVNIASKMGFTLSHSDSLAQOREHIELFRARKLAKSLAILLAFA 312  
Db 317 PR---SLKRGSKPSASSASLEKRMKMSQS-----ITQR--FRLSRDKKVAKSLAIVSIF 367  
Qy 313 AICWAPYSLTIVYISFFPERNLTKSTWYHTAFWLOWNSFVNPLYPLCHKRFOKAFKIL 372  
Db 368 GLCWAPYTLMIIRAAACHGRCI-PDYWYETSFVLLWANSVNPVLYPLCHHSFRRAFTKL 426  
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Db 427 LCPQKLKVQPH 437

Search completed: April 27, 2006, 05:44:16  
Job time : 47 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:54:06 ; Search time 165 Seconds  
(without alignment)  
985.064 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANSTIALTSIKISLTLFL.....LKILPVRQSTPPHNRISIST 389

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2036	100.0	389	5	US-10-626-445-10
2	2036	100.0	389	5	US-10-626-126-10
3	2036	100.0	389	5	US-10-626-398-10
4	1308.5	64.3	390	3	US-09-812-216-2
5	1308.5	64.3	390	3	US-09-910-411-2
6	1308.5	64.3	390	3	US-09-875-076-14
7	1308.5	64.3	390	3	US-09-876-252-14
8	1308.5	64.3	390	3	US-09-852-165-2
9	1308.5	64.3	390	3	US-09-891-138A-6
10	1308.5	64.3	390	4	US-10-052-193-2
11	1308.5	64.3	390	4	US-10-225-567A-629
12	1308.5	64.3	390	4	US-10-272-983-14
13	1308.5	64.3	390	4	US-10-354-769-2
14	1308.5	64.3	390	4	US-10-393-807-14
15	1308.5	64.3	390	4	US-10-417-820A-14
16	1308.5	64.3	390	4	US-10-349-253A-2
17	1308.5	64.3	390	4	US-10-696-673-2
18	1308.5	64.3	390	4	US-10-723-955-14
19	1308.5	64.3	390	4	US-10-782-596-14
20	1308.5	64.3	390	4	US-10-737-619-2
21	1308.5	64.3	390	5	US-10-626-445-2
22	1308.5	64.3	390	5	US-10-684-206-20
23	1308.5	64.3	390	5	US-10-616-088-2
24	1308.5	64.3	390	5	US-10-626-126-2
25	1308.5	64.3	390	5	US-10-626-398-2
26	1308.5	64.3	390	5	US-10-756-149-4702
27	1308.5	64.3	390	5	US-10-723-955-14

28	1308.5	64.3	390	5	US-10-488-421-8
29	1306.5	64.2	390	4	US-10-290-078-27
30	1306.5	64.2	390	5	US-10-488-421-6
31	1237	60.8	391	5	US-10-626-445-8
32	1237	60.8	391	5	US-10-626-126-8
33	1237	60.8	391	5	US-10-626-398-8
34	1236.5	60.7	391	5	US-10-626-445-9
35	1236.5	60.7	391	5	US-10-626-126-9
36	1236.5	60.7	391	5	US-10-626-398-9
37	1166	57.3	357	5	US-10-488-421-4
38	1048.5	51.5	336	5	US-10-488-421-2
39	694.5	34.1	413	3	US-09-891-053-1
40	694.5	34.1	413	5	US-10-759-463-1
41	689.5	33.9	445	3	US-09-350-206-2
42	689.5	33.9	445	3	US-09-349-755-2
43	689.5	33.9	445	3	US-09-166-334-2
44	689.5	33.9	445	4	US-10-282-958-2
45	689.5	33.9	445	4	US-10-225-567A-549

ALIGNMENTS

RESULT 1  
US-10-626-445-10  
; Sequence 10, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICATOR: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 10  
; LENGTH: 389  
; TYPE: PRT  
; ORGANISM: Cavia porcellus  
; US-10-626-445-10

Query Match	100.0%;	Score 2036;	DB 5;	Length 389;
Best Local Similarity	100.0%;	Pred. No. 7.6e-170;		
Matches 389;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLANSTIALTSIKISLTLFLMSLLAIAMLGNNVILAFIVDRNLHRSNYFPLNLAIAAD	60	
Db	1	MLANSTIALTSIKISLTLFLMSLLAIAMLGNNVILAFIVDRNLHRSNYFPLNLAIAAD	60	
QY	61	FPVGAIAIPLYIPSSLTWTSGKQACVFWLIITDYLLCTASVNVILISVDYRQSVSNVW	120	
Db	61	FPVGAIAIPLYIPSSLTWTSGKQACVFWLIITDYLLCTASVNVILISVDYRQSVSNVW	120	
QY	121	YRAQHSQGWKIATQWVAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKYFALPTSLL	180	
Db	121	YRAQHSQGWKIATQWVAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKYFALPTSLL	180	
QY	181	EPLIPILVAVPSAHYWSLWKREKLSRCLSHPVLPSSGSSSDHGHSCRDQPSRATLPA	240	
Db	181	EPLIPILVAVPSAHYWSLWKREKLSRCLSHPVLPSSGSSSDHGHSCRDQPSRATLPA	240	
QY	241	RKETTASLGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLAQOREHIELFRANK	300	
Db	241	RKETTASLGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLAQOREHIELFRANK	300	
QY	301	LAKSLAILLAAPAI CWAPYSLTTVIYSFPPERNLTGKSTWYHTAFMLQWFNSFVNPFLYPL	360	
Db	301	LAKSLAILLAAPAI CWAPYSLTTVIYSFPPERNLTGKSTWYHTAFMLQWFNSFVNPFLYPL	360	

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Qy 361 CHRFQKAFKILPVRROSTPPHNRISST 389
Db 361 CHRFQKAFKILPVRROSTPPHNRISST 389

RESULT 2
US-10-626-126-10
; Sequence 10, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-126-10

Query Match 100.0%; Score 2036; DB 5; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLANNSTIALTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFFLNLAIAD 60
Db 1 MLANNSTIALTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFFLNLAIAD 60
Qy 61 FVGAIAIPLYPSSLTWTSGKQACVFMLITDYLLCTASVNVIVLISYDRYQSVNAVM 120
Db 61 FVGAIAIPLYPSSLTWTSGKQACVFMLITDYLLCTASVNVIVLISYDRYQSVNAVM 120
Qy 121 YRAQSGTWKIATQMAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
Db 121 YRAQSGTWKIATQMAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
Qy 181 EFLPILLVAVFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHGHSCRODPDSRATLPA 240
Db 181 EFLPILLVAVFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHGHSCRODPDSRATLPA 240
Qy 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIELFRARK 300
Db 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIELFRARK 300
Qy 301 LAKSLAILLAFAICWAPYSLTIVYISFFPERNLTKSTWYHTAFWLQWFNFSFVNPFLYPL 360
Db 301 LAKSLAILLAFAICWAPYSLTIVYISFFPERNLTKSTWYHTAFWLQWFNFSFVNPFLYPL 360
Qy 361 CHRFQKAFKILPVRROSTPPHNRISST 389
Db 361 CHRFQKAFKILPVRROSTPPHNRISST 389

RESULT 3
US-10-626-398-10
; Sequence 10, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Cavia porcellus
US-10-626-398-10

Query Match 100.0%; Score 2036; DB 5; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.6e-170;
Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLANNSTIALTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFFLNLAIAD 60
Db 1 MLANNSTIALTSIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRNSNYFFFLNLAIAD 60
Qy 61 FVGAIAIPLYPSSLTWTSGKQACVFMLITDYLLCTASVNVIVLISYDRYQSVNAVM 120
Db 61 FVGAIAIPLYPSSLTWTSGKQACVFMLITDYLLCTASVNVIVLISYDRYQSVNAVM 120
Qy 121 YRAQSGTWKIATQMAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
Db 121 YRAQSGTWKIATQMAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSL 180
Qy 181 EFLPILLVAVFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHGHSCRODPDSRATLPA 240
Db 181 EFLPILLVAVFSAHIYWSLWKREKLSRCLSHPVLPDSSSSSDHGHSCRODPDSRATLPA 240
Qy 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIELFRARK 300
Db 241 RKTETASLGSDKSRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLALQOREHIELFRARK 300
Qy 301 LAKSLAILLAFAICWAPYSLTIVYISFFPERNLTKSTWYHTAFWLQWFNFSFVNPFLYPL 360
Db 301 LAKSLAILLAFAICWAPYSLTIVYISFFPERNLTKSTWYHTAFWLQWFNFSFVNPFLYPL 360
Qy 361 CHRFQKAFKILPVRROSTPPHNRISST 389
Db 361 CHRFQKAFKILPVRROSTPPHNRISST 389

RESULT 4
US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
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Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;  
QY 5 NSTIALT-SIKLSLFLMSLLAIAIMGNVVILAFIVDRNLRHSNTFFFLMLAIDFFV 63  
Db 5 NSTINLSLSTRVTLAFPMVSLVAFALMGNALVILAFVVDKRLRHSSYFFFLMLAIDFFV 64  
QY 64 GAIAIPLXIPSSLTWTSGKQACVFWLITDYLLCTASVNVNVLISYDRVQSVSNVAVYRA 123  
Db 65 GVISIPLIPIHPLFEWDFGKEICVFWLITDYLLCTASVNVNVLISYDRVLSVNAVSTRT 124  
QY 124 QHSGTWKIATQMAVWIFSPMTNGPMILISDSQNSITTECEPGFLKKYFALPTSLLEFL 183  
Db 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSBKDEGSECEPGFSEWVILAITSFLEFV 184  
QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCROPPDSRATLPARKE 243  
Db 185 IPVILVAYFNMIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFRGLSSRRSLASTE 243  
QY 244 TTASIGSDKSRKSSILPSIRAYKSNVIAKMGFLSHSDSLAQORSHIELFRARKLAK 303  
Db 244 VPASFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRARLAK 303  
QY 304 SLAIIILAAFAICWAPYSLTIVSYFFPBRNLTSTWYHTAFWLQWNSFVNPFLYPLCHK 363  
Db 304 SLAIIILGVAVCAWAPYSLTIVSYSSATGPKSVWYRIAFWLQWNSFVNPFLYPLCHK 363  
QY 364 RFQKAFKLKILPVRRQSTP-PHNRISIT 389  
Db 364 RFQKAFKLKIFCIKQKPLPSQHSRVS 390

## RESULT 5

US-09-910-411-2  
; Sequence 2, Application US/09910411  
; Patent No. US20020137054A1  
; GENERAL INFORMATION:  
; APPLICANT: Bergema, Derek  
; APPLICANT: Fitzgerald, Laura  
; APPLICANT: Li, Xiatong  
; APPLICANT: Michalovich, David  
; APPLICANT: Zhu, Yuan  
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
; FILE REFERENCE: GPT0655-2C1  
; CURRENT APPLICATION NUMBER: US/09/910,411  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: 09/693,761  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/497,790  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/431,898  
; PRIOR FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-910-411-2

Query Match 64.3%; Score 1308.5; DB 3; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.6e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKLSLFLMSLLAIAIMGNVVILAFIVDRNLRHSNTFFFLMLAIDFFV 63  
Db 5 NSTINLSLSTRVTLAFPMVSLVAFALMGNALVILAFVVDKRLRHSSYFFFLMLAIDFFV 64  
QY 64 GAIAIPLXIPSSLTWTSGKQACVFWLITDYLLCTASVNVNVLISYDRVQSVSNVAVYRA 123  
Db 65 GVISIPLIPIHPLFEWDFGKEICVFWLITDYLLCTASVNVNVLISYDRVLSVNAVSTRT 124  
QY 124 QHSGTWKIATQMAVWIFSPMTNGPMILISDSQNSITTECEPGFLKKYFALPTSLLEFL 183  
Db 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSBKDEGSECEPGFSEWVILAITSFLEFV 184

Db 125 QHTGVLKIVTLMAVWVLAFLVNGPMILVSBKDEGSECEPGFSEWVILAITSFLEFV 184  
QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCROPPDSRATLPARKE 243  
Db 185 IPVILVAYFNMIYWSLWKRDHLSCQHPGLTA-VSSNICGHSFRGLSSRRSLASTE 243  
QY 244 TTASIGSDKSRKSSILPSIRAYKSNVIAKMGFLSHSDSLAQORSHIELFRARKLAK 303  
Db 244 VPASFHSERQRRKSSLMFSSRTKNSNTIASKMGFSQSDSVLHQREHVELLRARLAK 303  
QY 304 SLAIIILAAFAICWAPYSLTIVSYFFPBRNLTSTWYHTAFWLQWNSFVNPFLYPLCHK 363  
Db 304 SLAIIILGVAVCAWAPYSLTIVSYSSATGPKSVWYRIAFWLQWNSFVNPFLYPLCHK 363  
QY 364 RFQKAFKLKILPVRRQSTP-PHNRISIT 389  
Db 364 RFQKAFKLKIFCIKQKPLPSQHSRVS 390

## RESULT 6

US-09-875-076-14  
; Sequence 14, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,127  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/141,448  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,633  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,555  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,282

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; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match      64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

Qy 5 NSTALT-SIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSSNYFFLNLAIDFFV 63
Db 5 NSTINLSLSTRVTTLAFPFMSLVAFALMGNALVILAFVVDKLNLRSSYFFLNLAISDFFV 64

Qy 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYINVLISYDRYQSVSNVAVRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYINVLISYDRYLSVSNVAVSRT 124

Qy 124 QHSGTWKIATQWAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSLLEFL 183
Db 125 QHTGVKIVTLWVAVWVLAFLVNGPMILVSESWKDEGCEGPGFSEWYILAITSFLEFV 184

Qy 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCRODPPDSRATLPARKE 243
Db 185 IPVLIVAFYNNIYWSLWKRDHLRCQSHPLGTA-VSSNICGHSFRGLSSRRSLASTE 243

Qy 244 TTASLGDSKRRKSLPISIRAYKXNSNVIAASKMGFLSHSDSLAQOREHIELFARKLAK 303
Db 244 VPASFHSERQRRKSLMFSSTKXNSNTIASKMGSPQSOSDVALHQREHVELLARLAK 303

Qy 304 SLAILLAFAFCWAPYSITTVIYGFPPERNITKSTWHTAFWLQWFSNVNPFYPLCHK 363
Db 304 SLAILLGVAFCWAPYSITFTVLFSYSSATGPKSVYRIAFWLQWFSNVNPFYPLCHK 363

Qy 364 RFQKAFKILVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKIFCIKQKPLPSQHSRVS 390

RESULT 7
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liew, Chen W
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876.252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match      64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

Qy 5 NSTALT-SIKISITFLMSLLAIAIMLGNNVVILAFIVDRNLHRSSNYFFLNLAIDFFV 63
Db 5 NSTINLSLSTRVTTLAFPFMSLVAFALMGNALVILAFVVDKLNLRSSYFFLNLAISDFFV 64

Qy 64 GAIAIPLYIPSSLTWTSGKQACVFWLITDYLLCTASVYINVLISYDRYQSVSNVAVRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYINVLISYDRYLSVSNVAVSRT 124

Qy 124 QHSGTWKIATQWAVWIFSFMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSLLEFL 183
Db 125 QHTGVKIVTLWVAVWVLAFLVNGPMILVSESWKDEGCEGPGFSEWYILAITSFLEFV 184

Qy 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPLVPSDSSSDHGHSCRODPPDSRATLPARKE 243
Db 185 IPVLIVAFYNNIYWSLWKRDHLRCQSHPLGTA-VSSNICGHSFRGLSSRRSLASTE 243
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QY 244 TTASLGSDKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSEQRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTIVYSPFPPERNLTSTWYHTAFWLQWNSFVNPFLYPLCHK 363
Db 304 SLAIIIGVAVCWAPYSLTIVLSFYSSATGPKSVYRIAFWLQWNSFVNPFLYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 8
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind Peter
; APPLICANT: Sejltz, Torsten
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1 G Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: USN 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-165-2

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNNVVILAFIVDRNLHRHSYFFFLNLAIADPFV 63
Db 5 NSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKRLHRSSYFFFLNLAIADPFV 64
QY 64 GAIAIPLYPSSLTWTSGKQACVFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVAVYRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVAVYRT 124
QY 124 QHSGTWKIATQWAVWIFSPFMINGPMILISDQNSSTCEBPGFLKKWYFALPTSLLBFL 183
Db 125 QHTGVLTIVTLVAVWVLAFLVNGFPMILVSESKDEGECEPFPFSEWYILAITSFLEFV 184
QY 184 IPILLVAFSAHIYWSLWREKLSRCLSHVPLPSDSSSDHSGSCRPDPDSRATLPARKE 243
Db 185 IPVILVAFYNNIYWSLWKRDLHSLRCQSHPLGTA-VSSNICGHSFGRSLSRSSLSASTE 243
QY 244 TTASLGSDKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSEQRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTIVYSPFPPERNLTSTWYHTAFWLQWNSFVNPFLYPLCHK 363
Db 304 SLAIIIGVAVCWAPYSLTIVLSFYSSATGPKSVYRIAFWLQWNSFVNPFLYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 9
US-09-891-138A-6
; Sequence 6, Application US/09891138A
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; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match 64.3%; Score 1308.5; DB 3; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNNVVILAFIVDRNLHRHSYFFFLNLAIADPFV 63
Db 5 NSTINLSLSTRVTLAFVSLVAFALMGNALVILAFVVDKRLHRSSYFFFLNLAIADPFV 64
QY 64 GAIAIPLYPSSLTWTSGKQACVFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVAVYRA 123
Db 65 GVISIPLYIPHTLFEWDFGKEICVFWLITDYLLCTASVYVNIIVLSYDRYQSVSNVAVYRT 124
QY 124 QHSGTWKIATQWAVWIFSPFMINGPMILISDQNSSTCEBPGFLKKWYFALPTSLLBFL 183
Db 125 QHTGVLTIVTLVAVWVLAFLVNGFPMILVSESKDEGECEPFPFSEWYILAITSFLEFV 184
QY 184 IPILLVAFSAHIYWSLWREKLSRCLSHVPLPSDSSSDHSGSCRPDPDSRATLPARKE 243
Db 185 IPVILVAFYNNIYWSLWKRDLHSLRCQSHPLGTA-VSSNICGHSFGRSLSRSSLSASTE 243
QY 244 TTASLGSDKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
Db 244 VPASHSEQRQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLQREHVELLRARRLAK 303
QY 304 SLAIIAFAICWAPYSLTIVYSPFPPERNLTSTWYHTAFWLQWNSFVNPFLYPLCHK 363
Db 304 SLAIIIGVAVCWAPYSLTIVLSFYSSATGPKSVYRIAFWLQWNSFVNPFLYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
Db 364 RFQKAFKILPVRRQSTP-PHNRISIT 389

RESULT 10
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-052-193-2

Query Match      64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRHSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGNALVILAFVVDKMLHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYTWSGKQACVFWLITDYLCTASVNVNVLISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYLSVNAVSYRT 124

QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISDQWNSQNTTECEPGFKKQWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184

QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCRODPDSDRATLPARK 243
DB 185 IPVILVAFNNIYWSLWKRDHLSCQSHPLGTA-VSSNICGHSFGRGLSSRRSLASTE 243

QY 244 TTASIGSKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSSLMFSSRTKNSNTIAKMGFSQSDSVALHQREHVELLRARLAK 303

QY 304 SLAILLAFAICWAPYSLTTVIYSPFPERNLTKSTWHTAFWLQWFNSFVNPFLYPLCHK 363
DB 304 SLAILLGVAFCWAPYSLTFTVLVSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHK 363

QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
DB 364 RFQKAFKILFCIKKQPLPSQHSRSVSS 390

RESULT 11
US-10-225-567A-629
; Sequence 629, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-629

Query Match      64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRHSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGNALVILAFVVDKMLHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYTWSGKQACVFWLITDYLCTASVNVNVLISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYLSVNAVSYRT 124

QY 124 QHSGTWKIATQWAVWIFSPMTNGPMILISDQWNSQNTTECEPGFKKQWYFALPTSLLEFL 183
DB 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184

QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCRODPDSDRATLPARK 243
DB 185 IPVILVAFNNIYWSLWKRDHLSCQSHPLGTA-VSSNICGHSFGRGLSSRRSLASTE 243

QY 244 TTASIGSKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSSLMFSSRTKNSNTIAKMGFSQSDSVALHQREHVELLRARLAK 303

QY 304 SLAILLAFAICWAPYSLTTVIYSPFPERNLTKSTWHTAFWLQWFNSFVNPFLYPLCHK 363
DB 304 SLAILLGVAFCWAPYSLTFTVLVSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHK 363

QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
DB 364 RFQKAFKILFCIKKQPLPSQHSRSVSS 390
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DB 125 QHTGVLKIVTLWVAVVWVLAFLVNGPMILVSESWKDEGSECEPGFSEWYIILAITSFLEFV 184
QY 184 IPILLVAFSAHIYWSLWKREKLSRCLSHPVLPDSSSSDHGHSCRODPDSDRATLPARK 243
DB 185 IPVILVAFNNIYWSLWKRDHLSCQSHPLGTA-VSSNICGHSFGRGLSSRRSLASTE 243
QY 244 TTASIGSKRRKSSLLPSIRAYKNSNVIAKMGFLSHSDSLAQOREHIELFRARKLAK 303
DB 244 VPASFHSERQRRKSSLMFSSRTKNSNTIAKMGFSQSDSVALHQREHVELLRARLAK 303
QY 304 SLAILLAFAICWAPYSLTTVIYSPFPERNLTKSTWHTAFWLQWFNSFVNPFLYPLCHK 363
DB 304 SLAILLGVAFCWAPYSLTFTVLVSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLYPLCHK 363
QY 364 RFQKAFKILPVRRQSTP-PHNRISIT 389
DB 364 RFQKAFKILFCIKKQPLPSQHSRSVSS 390

RESULT 12
US-10-272-983-14
; Sequence 14, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-14

Query Match      64.3%; Score 1308.5; DB 4; Length 390;
Best Local Similarity 65.1%; Pred. No. 4.6e-106;
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKISLTFMLSLAIAIMLGNVVVILAFIVDRNLHRHSNYFFFLNLAIDPFV 63
DB 5 NSTINLSLSTRVTLAFVMSLAFALMGNALVILAFVVDKMLHRSSYFFFLNLAISDFV 64

QY 64 GAIAIPLYPSSLTYTWSGKQACVFWLITDYLCTASVNVNVLISYDRYQSVNAVWYRA 123
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYLSVNAVSYRT 124
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QY 124 OHSGETWKIATQWAVVWIFPSMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSILREPL 183  
DB 125 QHTGVLKIVTLMAVAVVLAFLVNGPMILVSESKDGESECEPGFSEWYFALPTSILREPL 184  
QY 184 IPILLVAYPSAHYIYMSLWREKLSRCLSHPVLPDSOSSSDHGHSCRDQDPSRATLIPARKE 243  
DB 185 IPVILVAYFNMNIYMSLWKRDLHSLRCQSHPLGTA-VSSNICGHSFRGLSSRRSLASST 243  
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLALQOREHIELFRARKLAK 303  
DB 244 VPASPHSERQRRKSSLMFSSRTKNSNTTASKMGSPSQSDSVLHQREHVELLRARLAK 303  
QY 304 SLAIIILAAFAICWAPYSLTIVLSPERNLTKSTWYHTAFWLQWNSFVNPLPLCHK 363  
DB 304 SLAIIILGFAVCWAPYSLTIVLSPERNLTKSTWYHTAFWLQWNSFVNPLPLCHK 363  
QY 364 RFQKAPLKLPLVRRQSTP-PHNRISST 389  
DB 364 RFQKAPLKLPLFCIKKQPLPSQHSRSVSS 390

## RESULT 13

US-10-354-769-2  
; Sequence 2, Application US/10354769  
; Publication No. US20030149242A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: O'Reilly, Mark A.  
; APPLICANT: Peter, Beate  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
; FILE REFERENCE: PC10373B  
; CURRENT APPLICATION NUMBER: US/10/354,769  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 09/698,801  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/211,243  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: GB 9925641.4  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: GB 0009973.9  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-354-769-2

Query Match 64.3%; Score 1308.5; DB 4; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.6e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKSLTFLMSLAIAMGNVVLAFIVDRNLRHNSVFFFLNLAIDPFV 63  
DB 5 NSTINLSLSTRVTLTAFFMSLVAFAIMLGNALVILAFVVDKNNRHSRVSFFFLNLAIDPFV 64  
QY 64 GAIAIPLYIPSSLTWYTSKQACVFWLITDYLCTASVNVNVLISYDRYQSVSNVAVYRA 123  
DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYQSVSNVAVYRA 124  
QY 124 QHSGETWKIATQWAVVWIFPSMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSILREPL 183  
DB 125 QHTGVLKIVTLMAVAVVLAFLVNGPMILVSESKDGESECEPGFSEWYFALPTSILREPL 184  
QY 184 IPILLVAYPSAHYIYMSLWREKLSRCLSHPVLPDSOSSSDHGHSCRDQDPSRATLIPARKE 243  
DB 185 IPVILVAYFNMNIYMSLWKRDLHSLRCQSHPLGTA-VSSNICGHSFRGLSSRRSLASST 243  
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLALQOREHIELFRARKLAK 303  
DB 244 VPASPHSERQRRKSSLMFSSRTKNSNTTASKMGSPSQSDSVLHQREHVELLRARLAK 303

QY 304 SLAIIILAAFAICWAPYSLTIVLSPERNLTKSTWYHTAFWLQWNSFVNPLPLCHK 363  
DB 304 SLAIIILGFAVCWAPYSLTIVLSPERNLTKSTWYHTAFWLQWNSFVNPLPLCHK 363  
QY 364 RFQKAPLKLPLVRRQSTP-PHNRISST 389  
DB 364 RFQKAPLKLPLFCIKKQPLPSQHSRSVSS 390

## RESULT 14

US-10-393-807-14  
; Sequence 14, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huang T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-393-807-14

Query Match 64.3%; Score 1308.5; DB 4; Length 390;  
Best Local Similarity 65.1%; Pred. No. 4.6e-106;  
Matches 252; Conservative 48; Mismatches 84; Indels 3; Gaps 3;

QY 5 NSTIALT-SIKSLTFLMSLAIAMGNVVLAFIVDRNLRHNSVFFFLNLAIDPFV 63  
DB 5 NSTINLSLSTRVTLTAFFMSLVAFAIMLGNALVILAFVVDKNNRHSRVSFFFLNLAIDPFV 64  
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DB 65 GVISIPLYIPHTLPEWDFGKEICVFWLITDYLCTASVNVNVLISYDRYQSVSNVAVYRA 124  
QY 124 QHSGETWKIATQWAVVWIFPSMTNGPMILISDSWQNSTTECEPGFLKKWYFALPTSILREPL 183  
DB 125 QHTGVLKIVTLMAVAVVLAFLVNGPMILVSESKDGESECEPGFSEWYFALPTSILREPL 184  
QY 184 IPILLVAYPSAHYIYMSLWREKLSRCLSHPVLPDSOSSSDHGHSCRDQDPSRATLIPARKE 243  
DB 185 IPVILVAYFNMNIYMSLWKRDLHSLRCQSHPLGTA-VSSNICGHSFRGLSSRRSLASST 243  
QY 244 TTASLGSDKSRKSSLLPSIRAYKSNVNTASKMGFLSHSDSLALQOREHIELFRARKLAK 303





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OM protein - protein search, using sw model

Run on: April 27, 2006, 05:55:16 ; Search time 26 Seconds  
(without alignments)  
680.419 Million cell updates/sec

Title: US-10-626-398-10  
Perfect score: 2036  
Sequence: 1 MLANNSTIALSIKISLTL.....LKILPVRQSTPPHNRISIST 389

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /SIDSS/prodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /SIDSS/prodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /SIDSS/prodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /SIDSS/prodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /SIDSS/prodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 6: /SIDSS/prodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /SIDSS/prodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /SIDSS/prodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	689.5	33.9	445	US-11-115-564-1	Sequence 1, Appli
2	688.5	33.8	445	US-11-115-564-2	Sequence 2, Appli
3	681.5	33.5	445	US-11-115-564-3	Sequence 3, Appli
4	549	27.0	441	US-11-241-956-3	Sequence 3, Appli
5	403.5	19.8	590	US-11-124-368A-183	Sequence 183, App
6	403.5	19.8	590	US-11-127-877-54	Sequence 54, Appl
7	395.5	19.4	532	US-11-127-877-42	Sequence 42, Appl
8	386.5	19.0	487	US-11-249-847-582	Sequence 582, App
9	385.5	18.9	429	US-11-127-877-51	Sequence 51, Appl
10	385.5	18.9	466	US-11-127-877-50	Sequence 50, Appl
11	373	18.2	466	US-11-127-877-41	Sequence 41, Appl
12	370	18.2	400	US-10-499-210-2	Sequence 2, Appli
13	356.5	17.5	353	US-10-875-716-10	Sequence 10, Appl
14	340.5	16.7	350	US-11-165-024-3	Sequence 3, Appli
15	338	16.6	458	US-11-232-805-46	Sequence 46, Appl
16	338	16.6	480	US-10-521-162-40	Sequence 40, Appl
17	336	16.5	462	US-11-232-805-44	Sequence 44, Appl
18	322.5	15.8	450	US-11-232-805-26	Sequence 26, Appl
19	322.5	15.8	450	US-11-232-805-27	Sequence 27, Appl
20	314.5	15.4	447	US-11-232-805-8	Sequence 8, Appli
21	313	15.4	450	US-11-232-805-7	Sequence 7, Appli
22	304	14.9	458	US-10-877-346-51	Sequence 51, Appl
23	296.5	14.6	475	US-10-877-346-48	Sequence 48, Appl
24	294	14.4	446	US-11-166-412-67	Sequence 67, Appl
25	292.5	14.4	365	US-11-875-716-9	Sequence 9, Appli

#### ALIGNMENTS

##### RESULT 1

US-11-115-564-1  
; Sequence 1, Application US/11115564  
; Publication No. US20050267116A1

##### GENERAL INFORMATION:

; APPLICANT: Peschke, Bernd  
; APPLICANT: Hohlwes, Rolf  
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,  
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND  
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A]AZEPINES  
; FILE REFERENCE: 6483.200-US  
; CURRENT APPLICATION NUMBER: US/11/115,564  
; CURRENT FILING DATE: 2005-04-27

; PRIOR APPLICATION NUMBER: US 60/387,047  
; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863  
; PRIOR FILING DATE: 2002-06-06

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1

; LENGTH: 445  
; TYPE: PRT

; ORGANISM: Homo Sapiens  
US-11-115-564-1

Query Match	33.9%	Score	689.5;	DB	7;	Length	445;
Best Local Similarity	37.3%	Pred. No.	1.4e-54;				
Matches	161;	Conservative	70;	Mismatches	132;	Indels	69;
Gaps	13;						

QY 3 ANNSTIATSIKISITFLMSLLAIIMLGWVVIATFVDRLHRSNYFFLNLAIDPF 62  
DB 26 ARGSAATAV---LAALMALLIVATVIGNALVMLAFVADSLRTQNNFFLNLAISDFL 82  
QY 63 VCAIAPIYIPSSLT-YMTSGKQACVFWLITDYLCTASVYVNIIVLISYDRYQSVSNVWY 121  
DB 83 VGAFICPIYVYVLTGRTFTGRLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRVSY 142  
QY 122 RAQHSQTKIATQWVAVMIFSPMTNGPMLISDSWQ-----NSTTE--CEPGFLKKWYPA 174  
DB 143 RAQQGDTRAVRKMLLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCAEFYNNWYEL 199  
QY 175 LPTSLLLEFLIPIIVAYFSAHYNSLWREKL-----SRCLSHPVLPSSSSS----- 222  
DB 200 ITASTLEFPTPLSVTFNLSIYLNIOQRTRLRLDGNAREAGPEPFPPEAQPSPPPPGCW 259  
QY 223 -----DHGHSRCQDDPSR-----ATL-----PARKETTASIGSDK 252  
DB 260 GCWQKRGHEAM---PLHRYGVGEAAVGAAGENTLGGGGGGSVASPTSSSSSSSRGTER 316





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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-54

Query Match      19.8%; Score 403.5; DB 7; Length 590;
Best Local Similarity 23.1%; Pred No. 1.4e-28;
Matches 124; Conservative 83; Mismatches 146; Indels 183; Gaps 16;

QY 15 ISLTFLMSLLAIAIMLGNVVVILAFIVDRNLHRHSNFFFLNLAIADFPVGAIAIPLYIPS 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 VFIAPLTGILALVTIIGNILVIVSPKVNQLTKVNNYVLLSLACADLLIIGVSMNLP--- 125

QY 75 SLTY-----WTSGKQACVFWLITDYLLCTASVNIIVLSIDRYQSVSNVAVYRAQHSWT 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 -TTVIIMRWALGNLACDLWLALDYVNASVNMNLLVLSFDYFSITRPLTYRAKR--TT 182

QY 130 KIATQWAV-WIFSMTNGPMILISDSWNSTT-----ECEPGFLKWKYFALPTSLLFLI 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 KRAGWIGLAWIVSFLWAPAILFWQYFVGKRTVPPGECFIOPLSEPTITFTGTALAFYM 242

QY 185 PILVAVPSAHYNSLWK-----LSHPVLPSDSSSDH----- 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 PVTIMTI---LYWRIYKETKRTKELAGLQASGTEAETENFVHPTGSSRSSSVYELQQ 298

QY 203 -----REKLSRC-----LSHPVLPSDSSSDH----- 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 SMKRSNRKRYGRCHFMTTKSWKPSSEQMDQDHSSSDSNWNDAASLNSASSDEEDIG 358

QY 225 -----GHSC-----RQD----- 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 SETRAIYIVLKLPGHSITLNSTKLPSSDNLOVPEEELGMDLERKADKLAQAKSVDDGG 418

QY 232 --PDSRATLPARKET-----TASIGSDKSRKSSLLPSIRAYKSNVSIASKMGFLSHD 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 SFPKSFSLPIQLESADVDTAKTSDNVSSVGKSTATPLPSFK---EATLAKRFALKTRSQ 474

QY 284 SLALQOREHIELFRARKLAKSLAILLAAPALCWAPYSLTITVIYFFPERNLTKSTWHTA 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 ---ITKRKMSLVKREKKAQTLSAILLAFITWTTPYNI-MVLVSTFCDKCPVTLW-HLGWYLCVYVNSTVNP 529

QY 344 FWLQWFSFVNPFLYPLCHKRFKAFKILPV-----RRQSTPPHNS 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 530 YWLCYINSTVNPVCYALCNKTRFTTFMILLCCQCKKRRKQYQORQSVLFHKRA 585

RESULT 7
US-11-127-877-42
; Sequence 42, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. P.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-42
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Query Match      19.4%; Score 395.5; DB 7; Length 532;
Best Local Similarity 24.2%; Pred No. 6.7e-28;
Matches 121; Conservative 79; Mismatches 145; Indels 155; Gaps 16;

QY 15 ISLTFLMSLLAIAIMLGNVVVILAFIVDRNLHRHSNFFFLNLAIADFPVGAIAIPLYIPS 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 ITIAAVTAVSLITIVGNLVWISFKVNSQLTKVNNYVLLSLACADLLIIGVSMNLY--- 87

QY 75 SLTY-----WTSGKQACVFWLITDYLLCTASVNIIVLSIDRYQSVSNVAVYRAQHSWT 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 88 -TTIYLMGRWALGSLACDLWLALDYVNASVNMNLLVLSFDYFSITRPLTYRAKR--TP 144

QY 130 KIATQWAV-WIFSMTNGPMILISDSWNSTT-----STTECEPGFLKWKYFALPTSLL 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 KRAGIMIGLAWILSIFLWAPAIL---CWQYLVGKRTVPLDCCQIOPLSEPTITFTGTAA 201

QY 182 FLIPILVAVPSAHY----- 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 FVIVSVMTIYLCRIYRETEKRTKDLADLOGSDSVTKAEKRPAPRALFRSCLRCRPTL 261

QY 198 -----NSL----- 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 AQERNOQASWSSSSRRSTSTTGKPSQATGPSANWAKAEQLATTCSSYP-----SSEDEK 315

QY 228 C-----RODPDSRATLPARKETTASLGSDKS--RRKSSLLPSIRAY--KNSN 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 316 ATDPVLQVYVYKQKESPGBEFSABETEETVTKAETEKSDYDTPNYLLSPAARHPKSK 375

QY 271 VIASKMGFLSHD----- 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 376 CVAYKFLVVKADGNQOETNGCHKVKIMPCPPVAKBPSTKGLNPNPSHOMTKRKRVLV 435

QY 297 RARKLAKSLAILLAAPALCWAPYSLTITVIYFFPERNLTKSTWHTAFWLQWFSFVNP 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 436 KERKAAQTLSAILLAFITWTTPYNI-MVLVSTFCDKCPVTLW-HLGWYLCVYVNSTVNP 493

QY 357 LYPLCHKRFKAFKILPV 376
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 494 CYALCNRTFRKTFKMLLCR 513

RESULT 8
US-11-249-847-582
; Sequence 582, Application US/11249847
; Publication No. US20060035270A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Kun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng
; APPLICANT: Benkovic, Stephen J.
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
; FILE REFERENCE: EPTM-P05-001
; CURRENT APPLICATION NUMBER: US/11/249,847
; CURRENT FILING DATE: 2005-10-12
; PRIOR APPLICATION NUMBER: 10/436,549
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
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; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 582
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-249-847-582.

Query Match      19.0%; Score 386.5; DB 7; Length 487;
Best Local Similarity 23.2; Pred. No. 3.9e-27;
Matches 114; Conservative 85; Mismatches 158; Indels 135; Gaps 14;

QY      1  MLANNSTIAITSIKISITELMSLAIAIMLGNVVVILAFIDRNLNRHSNVFPLNLAID 60
DB      14  MCEGNKTMASPOLMPLVVLVITCLVTVGLNLLVLYAVRSERKLHTVGNLYIVLSLVD 73

QY      61  FFGAIAIP---LYIPSLTWTSGKQACVFLLITDYLLCTASVYINVLISYDIQSVSN 117
DB      74  LIVGAVVPMNIIYL---LMSKWSLGRPLCLFWLSMDYVASTASIFSIFILCIDAYRSVQQ 131

QY      118  AVMYRAQHSQTKIATQAVMWIPSPFWTNGPMILISDSWQNSTT----ECEPGLKKWYP 173
DB      132  PLRYLKYRTKTRASAT--ILGAWFLSFLWVPIPLGWNHFMQOTSVRREDKCEETDFYDVTWF 190

QY      174  ALPTSLEFLPIILLVAFSAHIY-----KLSRCLSHPYL----- 197
DB      191  KVMTAIFNLYPTLLMLWFYAKIYKAVRQHCQHRELINRSLPSFSEIKLRPNPKGDAXK 250

QY      198  -----WSLWKRE-----KLSRCLSHPYL----- 215
DB      251  PGKESPEVILKRPKDGAGGSVLKSPQTPKEMKSPVVFSGEDDREVDKLYCPLDIVHM 310

QY      216  --PSDSSSD-----HGHS--CRQDP---DSRATLPARKETTASLG 249
DB      311  QAAAEAGSSRDVAVNRSHGQKTDQGLNTHGASEISEDOMLGDSQFSRTSDSTTTETA 370

QY      250  SDRSRKSSLLPSIRAYKSNVIVASQVGL-----SHSDSLAQORHIELFRARKLAKS 304
DB      371  PGKGKLS-----GSNTGLDYIKFTWKRLRSHS---ROYVSGLHMRERKAAQ 416

QY      305  LAILLAFAICWAPYSLTTVIYSPFPERNLTKSTWYHTAFWLQFNFSVNPFLYPLCHKR 364
DB      417  LGFIMAAFLICWPIFYFFWVIAFC--KNCNEHLHMTTWLGYINSTLPLIYPLCNEH 474

QY      365  FOXAKFLKILFVR 376
DB      475  FKTKFKELIHR 486

RESULT 9
US-11-127-877-51
; Sequence 51, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: Amyloid-Beta Protein Production
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590

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; Publication No. US20050266522A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Amine Receptor
; FILE REFERENCE: PF188D1C2
; CURRENT APPLICATION NUMBER: US/10/875,716
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 09/988,745
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/314,006
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 08/467,559
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-716-10

Query Match 17.5%; Score 356.5; DB 6; Length 353;
Best Local Similarity 27.2%; Pred. No. 1.4e-24;
Matches 101; Conservative 66; Mismatches 139; Indels 65; Gaps 11;

QY 20 LMSLLAIAIMLGNVVILAFIVDRNLRHRSNYFFLNLAIAADPFVGAIAIP--LYIPSSLT 77
Db 31 LUTLLAVIVFGNVLCMAVSREKALQTTNYLIIVSLAVADLLVATLVFVWVIL--EVVG 89

QY 78 YMTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGTWKIATQVMA 137
Db 90 EKWFSRIHCDIFVTLDMVMCTASILNLCAISIDRYTAVAMPMLNYTRYSSKRRVTMISI 149

QY 138 VNIQFPMWNGMIL--ISDSWQNSQSTTECEPGFLKCKWTFALPTSLLEPLIPIILLVAYPSAH 196
Db 150 VVWLSPTISCPLLFGLNADONECIIANPAFV-----VYSSIVSVFVFPFIVTLVYIKI 203

QY 197 YNSLWKREKLSRCLSHPVLPSSSDSHGHSRQDPDSRATL--PARKETASLGSQSKR 254
Db 204 YIVLRERRK-----RVNFKSSRAFRH-----LRAPLKEARREN---GHAQKH 246

QY 255 RKSSLLPSIRAYKNNSVIAKMGFLSHSDSLAQQRHIELFRARKLAISLAIIAALPAI 314
Db 247 PKIAKIFELQTPNGKT-----RTSLKTSRRKLSQKKEKATQMLAIVLGVFI 296

QY 315 CWAPVSLT-----TVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFLYPLCH 362
Db 297 CWLPFPFTHILNHCDNIPPVLYSAFT-----WLGTVNSAVNPIIYTFN 342

QY 363 KPQKAPLAKIL 373
Db 343 IEFKRAFLKIL 353

RESULT 14
US-11-165-024-3
; Sequence 3, Application US/11165024
; Publication No. US20050266527A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
; FILE REFERENCE: PF187D1C2
; CURRENT APPLICATION NUMBER: US/11/165,024
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 10/006,394
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 09/228,420
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 08/465,971
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 350

; Publication No. US20050266522A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Amine Receptor
; FILE REFERENCE: PF188D1C2
; CURRENT APPLICATION NUMBER: US/10/875,716
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 09/988,745
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: US 09/314,006
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 08/467,559
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-716-10

Query Match 17.5%; Score 356.5; DB 6; Length 353;
Best Local Similarity 27.2%; Pred. No. 1.4e-24;
Matches 101; Conservative 66; Mismatches 139; Indels 65; Gaps 11;

QY 20 LMSLLAIAIMLGNVVILAFIVDRNLRHRSNYFFLNLAIAADPFVGAIAIP--LYIPSSLT 77
Db 31 LUTLLAVIVFGNVLCMAVSREKALQTTNYLIIVSLAVADLLVATLVFVWVIL--EVVG 89

QY 78 YMTSGKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGTWKIATQVMA 137
Db 90 EKWFSRIHCDIFVTLDMVMCTASILNLCAISIDRYTAVAMPMLNYTRYSSKRRVTMISI 149

QY 138 VNIQFPMWNGMIL--ISDSWQNSQSTTECEPGFLKCKWTFALPTSLLEPLIPIILLVAYPSAH 196
Db 150 VVWLSPTISCPLLFGLNADONECIIANPAFV-----VYSSIVSVFVFPFIVTLVYIKI 203

QY 197 YNSLWKREKLSRCLSHPVLPSSSDSHGHSRQDPDSRATL--PARKETASLGSQSKR 254
Db 204 YIVLRERRK-----RVNFKSSRAFRH-----LRAPLKEARREN---GHAQKH 246

QY 255 RKSSLLPSIRAYKNNSVIAKMGFLSHSDSLAQQRHIELFRARKLAISLAIIAALPAI 314
Db 247 PKIAKIFELQTPNGKT-----RTSLKTSRRKLSQKKEKATQMLAIVLGVFI 296

QY 315 CWAPVSLT-----TVIYSPFPERNLTKSTWYHTAFWLQWNSFVNPFLYPLCH 362
Db 297 CWLPFPFTHILNHCDNIPPVLYSAFT-----WLGTVNSAVNPIIYTFN 342

QY 363 KPQKAPLAKIL 373
Db 343 IEFKRAFLKIL 353

RESULT 15
US-11-232-805-46
; Sequence 46, Application US/11232805
; Publication No. US20060073508A1
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M.
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-42D
; CURRENT APPLICATION NUMBER: US/11/232,805
; CURRENT FILING DATE: 2005-09-22
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 46
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-232-805-46

Query Match 16.6%; Score 338; DB 7; Length 458;
Best Local Similarity 25.9%; Pred. No. 9e-23;
Matches 107; Conservative 82; Mismatches 160; Indels 64; Gaps 13;

QY 17 LTFMLSLAIAIMLGNVVILAFIVDRNLRHRSNYFFLNLAIAADPFVGAIAIPLYIPSSL 76
Db 54 LAAVVGLIVFTVWGNVLVIAVLTSRALRQPNLFLVSLASADILVATLVMPFSLANEL 113

QY 77 -TYWTSQKQACVFWLITDYLLCTASVYNIIVLSYDRYQSVSNVYRAQHSQGTWKIATOM 135
Db 114 MAYWFGQWCGYIALDVLFCTSSIVHLCAISLDRYWSVTQAVENLKRTPR-RVKATI 172

QY 136 VAVWIFSPMTNGPMILISDSWQNSQSTTECEPGFLKCKWTFALPTSLLEPLIPIILLVAYPSAH 195
Db 173 VAVWMLISAVISFPFLVSLYRQPDGAAYPCGLNDETWTYILSSCIGSFAPCLIMGLVYAR 232

QY 196 IYWSLWKREKLSRCLSH-----FVLPSDSS-----SSDHGHSRQDPDSRATLPA 240
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OM protein - nucleic search, using frame\_plus\_p2n model

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=/abss/Patents NA -QWTF=fastcap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCT=0  
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-HOST=abss02p -USER=US10626398 @CGN 1 1 512 @runat 26042006 101728 18662  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*  
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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1308.5	64.3	1173	3	US-09-414-010-1
2	1308.5	64.3	1173	3	US-09-812-216-1
3	1308.5	64.3	1173	3	US-09-875-076-13
4	694.5	34.1	1239	3	US-09-891-053-2
5	694.5	34.1	2700	3	US-09-891-053-5
6	689.5	33.9	1335	2	US-08-985-090-3
7	689.5	33.9	1335	3	US-09-165-543-3
8	689.5	33.9	1335	3	US-09-167-354-6
9	689.5	33.9	1335	3	US-09-642-855-6

10	689.5	33.9	1335	3	US-09-642-514-6	Sequence 6, Appli
11	689.5	33.9	1335	3	US-09-642-852-6	Sequence 6, Appli
12	689.5	33.9	2050	3	US-09-891-053-21	Sequence 21, Appl
13	689.5	33.9	2665	3	US-09-943-016-5059	Sequence 5059, Ap
14	689.5	33.9	2689	2	US-08-985-090-1	Sequence 1, Appli
15	689.5	33.9	2689	3	US-09-165-543-1	Sequence 1, Appli
16	689.5	33.9	2699	3	US-09-167-354-5	Sequence 5, Appli
17	689.5	33.9	2699	3	US-09-642-855-5	Sequence 5, Appli
18	689.5	33.9	2699	3	US-09-642-514-5	Sequence 5, Appli
19	689.5	33.9	2699	3	US-09-642-852-5	Sequence 5, Appli
20	681.5	33.5	1338	3	US-09-165-543-6	Sequence 6, Appli
21	681.5	33.5	1953	3	US-09-891-053-26	Sequence 26, Appli
22	681.5	33.5	3244	3	US-09-165-543-4	Sequence 4, Appli
23	609.5	29.9	1056	3	US-09-524-162-1	Sequence 1, Appli
24	546	26.8	1086	2	US-08-985-090-6	Sequence 6, Appli
25	546	26.8	1086	3	US-09-165-543-33	Sequence 33, Appli
26	546	26.8	2218	2	US-08-985-090-4	Sequence 4, Appli
27	546	26.8	2218	3	US-09-165-543-31	Sequence 31, Appli
28	403.5	19.8	1913	3	US-09-016-434-1314	Sequence 1314, Ap
29	398.5	19.6	1773	3	US-09-826-509-516	Sequence 516, App
30	397	19.5	2261	3	US-09-016-434-1176	Sequence 1176, Ap
31	392	19.3	1599	3	US-09-826-509-520	Sequence 520, App
32	389.5	19.1	1386	3	US-09-016-434-1339	Sequence 1339, Ap
33	388.5	19.1	1956	2	US-08-313-553-6	Sequence 6, Appli
34	388.5	19.1	1956	3	US-08-767-993-6	Sequence 1411, Ap
35	386.5	19.0	1742	3	US-09-016-434-1411	Sequence 11, Appli
36	385.5	18.9	2004	2	US-08-722-001-11	Sequence 1368, Ap
37	385.5	18.9	2290	3	US-09-016-434-1368	Sequence 5, Appli
38	385.5	18.9	2536	3	US-09-919-039-5	Sequence 512, App
39	384.5	18.9	1422	3	US-09-826-509-512	Sequence 159, App
40	384.5	18.9	4008	3	US-09-976-594-158	Sequence 5, Appli
41	384	18.9	1639	2	US-08-334-598-5	Sequence 5, Appli
42	384	18.9	1639	2	US-08-228-932-5	Sequence 5, Appli
43	384	18.9	1639	2	US-08-468-939-5	Sequence 5, Appli
44	384	18.9	1639	2	US-08-406-855A-5	Sequence 5, Appli
45	384	18.9	1639	2	US-08-722-190-5	Sequence 5, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-414-010-1  
; Sequence 1, Application US/09414010  
; Patent No. 6204017  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Jiang Xu  
; APPLICANT: Hedrick, Joseph A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Monama, Frederick J. Jr.  
; APPLICANT: Morse, Kelley L.  
; APPLICANT: Umland, Shelby P.  
; TITLE OF INVENTION: Histamine receptor  
; FILE REFERENCE: CN01069  
; CURRENT APPLICATION NUMBER: US/09/414,010  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-414-010-1

Alignment Scores:  
Pred. No.: 3.68e-129 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.5% Conservative: 48  
Best Local Similarity: 65.1% Mismatches: 84  
Query Match: 64.3% Indels: 3  
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-414-010-1 (1-1173)

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Db 73 GTAGCTTTGCTATAAATAGTAAAGTCTTTGGTCACTTTTGTAGCTTTTGGTGGACAA 132
Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTACATCGAAGTGTATTTTCTTAACCTTGGCCATCTCTGACTTCTTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCATCTCTTGTATCATCCCTCACAGCTGTTCGAATGGATTTTGGAAAG 252
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Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
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Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 323
Db 910 TCATGGCCATCTCTTAGGGGTTTTCGTGTTTGTGGGCTCCCATATCTCTCTTTCCACA 969
Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
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RESULT 2
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monisma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
Alignment Scores:
Pred. No.: 3,68e-129 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3
US-10-626-398-10 (1-389) x US-09-812-216-1 (1-1173)
Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAACATCAATTATCACTAAGCACTCGTGTACTTTAGCATTTTATGTCCTTA 72
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Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170
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## RESULT 4

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US-09-891-053-2
; Sequence 2, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
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; CURRENT APPLICATION NUMBER: US/09/891.053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-891-053-2
Alignment Scores:
Pred. No.: 8,19e-64 Length: 1239
Score: 694.50 Matches: 159
Percent Similarity: 55.4% Conservative: 66
Best Local Similarity: 39.2% Mismatches: 130
Query Match: 34.1% Indels: 51
DB: 3 Gaps: 12
US-10-626-398-10 (1-389) x US-09-891-053-2 (1-1239)
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Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCTGTGGCCACAGTACTGGGCAACGCGTGTCTGCTGCTCGCTTCGTGGCGGAT 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhe 62
Db 187 TCGAGCTCTCCGCCACCCAGAAACATCTTTCTGTCTCAACCTCGCCATCTCCGATCTCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrThrSer 81
Db 247 GTGGTGCTTCTGCATCCCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 306
Qy 82 GlyLysGlnAlaCysValPheTyrPheLeuThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGGGGCTCTGCAAGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 366
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Db 367 TTCAACATCTATCTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 426
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Db 427 AGGCGCCAGCAGGGGGACACGAGCGGCGTTCGGAAGATGCGACTGGTGGTGGTGGTGGTGG 486
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Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysIleTyrTyrPheAla 174
Db 538 GGCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTGCTGATCTTCTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 598 ATCAGGCGCTCCACCCCTCGAGTTCTTCAAGCCCTTCTCTCAGCGGTACCTTCTTCAACCTC 657
Qy 195 HisIleTyrThrSerLeuTyrLysArgGluLysLeu-----SerArgCysLeuSer 211
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Qy 212 HisProValLeuProSerAspSerSerSerSer----- 222
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Qy 238 LeuProAlaArgLysGluThrThraLaserLeuGlySerAspLysSerArgArgLysSer 257
Db 808 ATGCCGTTGCACAGCTCTGGCAGCTCTCAAGGGGCGCACTGAGAGGCCACGC----- 858
Qy 258 SerLeuLeuProSerIleArgAlaTyrlsAsnSerAsnValIleAlaserLysMetGly 277
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RESULT 5
US-09-891-053-5
; Sequence 5, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891.053
; PRIOR FILING DATE: 2001-09-17
; CURRENT APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (351)...(1589)
; NAME/KEY: misc_feature

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; LOCATION: (1)...(2700)
; OTHER INFORMATION: n = A,T,C or G
US-09-891-053-5

Alignment Scores:
Pred. No.: 2,93e-63 Length: 2700
Score: 694.50 Matches: 159
Percent Similarity: 55.4% Conservative: 66
Best Local Similarity: 39.2% Mismatches: 130
Query Match: 34.1% Indels: 51
DB: 3 Gaps: 12

US-10-626-398-10 (1-389) x US-09-891-053-5 (1-2700)
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 426 GCGCGCGGCTTCTCGGCTGCCTGGACCGCTGC-----CTGGCTGGCGCTCATGGCG 476
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 477 CTGCTCATGCTGGGCCACAGTACTGGGCAACGCGTGTCTCATGCTCGGCTTGTGGCGGAT 536
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrlsPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 537 TCGAGCTTCGCGCCACCCAGAACACTTCTTCTGTCTCAACCTCGCCATCTCCGACTTCTC 596
Qy 63 ValGlyAlaIleAlaIleProLeuTyrlsPheProSerSerLeuThr-----TyrlsTrpSer 81
Db 597 GTGGGTGCTTCTGCATCCCATTTGTAGTACCTATGTGTGCTGACCGCGCGTGGACCTTC 656
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrlsLeuLeuCysThrAlaSerVal 101
Db 657 GCGCGGGGCTCTGCAAGCTGTGGCTGGTGTAGTACCTACTGTGTGCTCTCTCGGTC 716
Qy 102 TyrAsnIleValLeuIleSerTyrlsAspArgTyrlsGlnSerValSerAsnAlaValTrpTyrls 121
Db 717 TTCACATCTGCTACTCATCAGTATGACGATTCCTGTGCTGCTGCTGCTGCTGCTGCTGCT 776
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 777 AGGCCCCAGAGGGGGACAGAGCGCGCTTCGGAAGATGGCACTGCTGTGGGTGTGTG 836
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 837 GCCTTCTGCTGTATGGCGCTGCCATCTCTG-----AGTTGGAGTACCTGTGTGCT 887
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTyrlsPheAla 174
Db 888 GGCAGTTCCATCCCGAGGGCCACTGTATGCTGAGTTCTTCTACAACTGGTACTTCTTC 947
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrlsPheSerAla 194
Db 948 ATCAGCGCTCCACCTCGAGTTCTTCAAGCGCTTCTCAGCGCTTCTCAGCGTCTCTTCAACCTC 1007
Qy 195 HisIleTyrlsTrpSerLeuTyrlsArgGluLysLeu-----SerArgCysLeuSer 211
Db 1008 AGCATCTACCTGAACATCCAGAGCGCACCGCGCTTCCGCTGTATGGGGCGCGTAGGCT 1067
Qy 212 HisProValLeuProSerAspSerSerSer----- 222
Db 1068 GGCACAGAACCCCAAGGCGCATGGCGGCC----- 1127
Qy 223 -----AspHisGlyHisSerCysArgGlnAapProAspSerArgAlaThr 237
Db 1128 GGCTGCTGGCCAAAGGCGCATGGCGGCC----- 1157
Qy 238 LeuProAlaArgLysGluThrThraLaserLeuGlySerAspLysSerArgArgLysSer 257
Db 1158 ATGCCGTTGCACAGCTCTGGCAGCTCTCAAGGGGCGCACTGAGAGGCCACGC----- 1208
Qy 258 SerLeuLeuProSerIleArgAlaTyrlsAsnSerAsnValIleAlaserLysMetGly 277
Db 1209 TCACTCAAAAGGGGCTCCAAAGCCATCAGCATCTTCTGAGCATCCCTGGAGAGCGCATGAAG 1268

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Qy 278 PheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHisIleGluLeuPheArg 297
Db 1269 ATGGTGCCAGAGC-----ATCACCCAGGC-----TTCCGGCTCTCGGG 1310
Qy 298 AlaArgIysLeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAla 317
Db 1311 GACAAAGAGGTGGCCAAAGTCGCTGCCCATCATCGTGAGCATCTTTGGGCTCTGCTGGCG 1370
Qy 318 ProTyrSerLeuThrValIleTyrSerPhePheProGluArgAsnLeuThrLysSer 337
Db 1371 CCGTACAGCTCCCTAAATGATCATCCGAGCTCTTGGCCATGCGCCGCTGCATC---CCCGAT 1427
Qy 338 ThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeu 357
Db 1428 TACTGGTAAGAGAGCTCTTCTGCTCTGTGGGCCCACTCGGCCGTCAACCCCGTCTC 1487
Qy 358 TyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArg 377
Db 1488 TACCACTGTGCCACTACAGCTTCGGCAGAGCCTTACCAAGCTCTCTGCCGCCAGAAG 1547
Qy 378 GlnSerThrProProHis 383
Db 1548 CTCAAGGTCCAGCCCCAC 1565

RESULT 6
US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)42-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
US-08-985-090-3

Alignment Scores: 1335
Pred. No.: 689.50
Score: 161

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Percent Similarity: 53.5%      Conservative: 70
Best Local Similarity: 37.3%    Mismatches: 132
Query Match: 33.9%             Indels: 69
DB: 2                           Gaps: 13

US-10-626-398-10 (1-389) x US-08-985-090-3 (1-1335)
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGGCTTCTCGGCAGCTCGACCGCGTG-----CTGGCGCGGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCTGTCGCGACCGTGTGGCAGCGTGTGTCATGCTCGCTTCTGTCGCGGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCCTCCGCCACCCAGAACACTTCTTCTCTCAACCTCGCCATCTCCGACTTCCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 247 GTGGCGCCTTCTGCATCCCACTGTATGTACCTACGTGTGACAGCGCGCTGGACCTTC 306
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGGGGCTCTGCAAGCTGTGGTGTAGTGCACCTACCTGTGTGCACCTCTCTCTGCC 366
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 367 TTCAACATCTGCTCATCATCAGTACGACCGCTTCTCTGCGGTCAACCGAGCGGTCTCATC 426
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 427 CGGGCCAGCAGCGGTGCACGCGCGGGCAGTGGGAGATGTGTGTGTGGTGGTGTGCTG 486
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 487 GCCTTCTGCTGTACGACCGACCATCTCTG-----AGCTGGGAGTACCTGTCCGGG 537
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysIleTyrPheAla 174
Db 538 GCGAGCTCCATCCCGGAGGCCACTGCTATGCGGAGTCTTCTACAACTGGTACTTCCTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaIlePheSerAla 194
Db 598 ATCAGCGTTCACCTCTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTC 657
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 658 AGCATCTACCTGAACATCCAGAGCGCACCGCGCTCGGCTGATGGGCTCGAGAGGCA 717
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 718 GCGCGCCCGAGCGCCCTTCCGAGGCCACGCTCCACCCACCGCTCGGTGTGTGG 777
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 778 GGCTGTGGCAGAGGGGCAAGGGGAGGCGCATG-----CCGCTGCACAGGTATGGG 828
Qy 236 -----AlaThrLeu----- 238
Db 829 GTGGGTGAGCGCGCTGAGCGCTGAGCGCGGAGCGGAGCGCTCGGGGGTGGCGTGG 888
Qy 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
Db 889 GCGGCTCGGTGCTTCAACCCACTCCAGCTCCGCGGAGCTCTCGAGGGGCACTGAGAGG 948
Qy 253 SerArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 949 CCGGCG-----TCACTCAAGAGGGGCTCCAGCGCTCGGCGTCTCTGGCTCACTG 999
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292

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Db 1000 GAGAGCGCATGAGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041  
Qy 293 lIeGluLeuPheAArgAlaArgLysLeuAlaLysSerLeuAlaLleLeuLeuAlaLaphe 312  
Db 1042 TTTCGGCTGTCTCGGACAGGAAAGTGCCAAAGTCGTGGCGGTATCGTGAGCATCTTT 1101  
Qy 313 AlaileCysTrpAlaProTyrSerLeuThrThrValileTyrSerPhePheProGluArg 332  
Db 1102 GGGCTCTGCTGGGCCCCATACAGCTGTGTGATCATCCGGCGCGCTGC---CATGGC 1158  
Qy 333 AenLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAasnSerPhe 352  
Db 1159 CACTGCGTCCCTGACTACTGTGTACGAAACCTCTTCTGGCTCTGTGGGCCCAACTGGCT 1218  
Qy 353 VallanProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysile 372  
Db 1219 GTCAACCTGTCTTACCTCTGTGTCACCACTTCGCGCGGCTTCACCAAGCTG 1278  
Qy 373 LeuProValArgArgGlnSerThrProProHisAen 384  
Db 1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGC 1314

## RESULT 7

US-09-165-543-3  
; Sequence 3, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,543  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1335  
US-09-165-543-3

Alignment Scores:  
Pred. No.: 3.15e-63 Length: 1335  
Score: 689.50 Matches: 161  
Percent Similarity: 53.5% Conservatism: 70  
Best Local Similarity: 37.3% Mismatches: 132

Query Match: 33.9% Indels: 69  
DB: 3 Gaps: 13  
US-10-626-398-10 (1-389) x US-09-165-543-3 (1-1335)  
Qy 3 AlaAasnAasnSerThrIleAlaLeuThrSerLysIleSerLeuThrPheLeuMetSer 22  
Db 76 GCGCGCGCTTCTCGGACGCTGGACCGCGTG-----CTGGCGCGCTCATGGCG 126  
Qy 23 LeuLeuAlaLleAlaLleMetLeuGlyAasnValValIleLeuAlaPheAlaValasp 42  
Db 127 CTGCTCATCGTGGCGACGCTGTGGCAACGCGTGTGTCTCATGCTCGCTTGTGGCCGAC 186  
Qy 43 ArgAasnLeuArgHisAArgSerAasnTyrPhePheLeuAasnLeuAlaLleAlaAasnPhePhe 62  
Db 187 TCGAGCTTCGCGACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTC 246  
Qy 63 ValGlyAlaLleAlaLleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81  
Db 247 GTCGCGCGCTTCTGCATCCCACTGTATGATACCTACCTGCTGACAGCGCGCTGGACCTTC 306  
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101  
Db 307 GCGCGGGCGCTCTGCAAGCTGTGGCTGTAGTGAACCTACCTGCTGTGCACCTCTCTGCC 366  
Qy 102 TyrAasnIleValleuIleSerTyrAspArgTyrGlnSerValSerAasnAlaValTrpTyr 121  
Db 367 TTCAACATCGTGTCTCATGACCTACGACCGCTTCTCTGCGGTACCCGCGCGGTCTCATAC 426  
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141  
Db 427 CGGCGCCAGCAGGTGTGACCGCGGGCGAGTGGGAAGATGCTGCTGTGGTGGGTGCTG 486  
Qy 142 SerPheMetThrAenGlyProMetIleLeuIleSerAspSerTrpGln----- 157  
Db 487 GCCTTCTGCTGTACGACGACGACCATCTG-----AGCTGGAGTACCTGTCCGGG 537  
Qy 158 ---AasnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPheAla 174  
Db 538 GGCAGCTCCATCCCGGAGGCGCACTGTATGCGCGAGTCTTCTTACAACTGTGTATCTCTC 597  
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTrpPheSerAla 194  
Db 598 ATCAGCGCTTCCACCTGGAGTCTTTACGCGCTTCTCTCAGCGTCACTCTTTTAACCTC 657  
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210  
Db 658 AGCATCTACCTGAACATCCAGAGCGCGCACCGCTCCGGCTGGATGGGCTCGAGAGGCA 717  
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222  
Db 718 GCGGCGCCCGAGCGCCCTCCGAGGCGCCAGCCCTCACACCCCGCCCTGGCTGTGGTGG 777  
Qy 223 -----AspHisGlyHisSerCysArgGlnAaspProAaspSerArg----- 235  
Db 778 GGCTGTGGCAGAAGGGGCAAGGGAGCGCATG-----CCGCTGCACAGATATGGG 828  
Qy 236 -----AlaThrLeu----- 238  
Db 829 GTGGGTGAGCGCGCGGTAGCGCTGAGCGCGGGAGGCGGACCTCGGGGGTGGCGGTGGG 888  
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuLysArgAspLys 252  
Db 889 GCGCGCTCCGTGGCTTCACCCACCTCCAGCTCCGCGGAGCTCTCCAGGGGCGACTGAGAGG 948  
Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAasnSerAasnValile 272  
Db 949 CCGCGC-----TCACTCAAGAGGGGTCCAGCGCGCTCGGGCGTCTCGGCTCTACTG 999  
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292  
Db 1000 GAGBAGCGCATGAGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041

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Qy 293 ILeGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLeuLeuAlaAlaPhe 312
Db 1042 TTTGGGCTGTCTCGGACAGAAAGTGCCAGTGGCTGGCCGCTCATCGTGAGCACTTT 1101
Qy 313 AlaLeuCystrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGGCTGTCTGGGCCCCCATACACGCTGTGATGATCATCGGGCGGCTGC---CATGGC 1158
Qy 333 AsnLeuThrLysSerThrTyrTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CACTCGCTCCCTGACTACTGTGTACAAACCTCTCTGTGGCTCTGTGGGCAACTCGGCT 1218
Qy 353 ValAsnProPheLeuTyrProLeuCyHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGTCTCTACCTCTGTGTGCACACAGCTTCCGGCGGCTTTCACCAAGCTG 1278
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1279 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGC 1314
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## RESULT 8

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US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 613659
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167.354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6
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Alignment Scores:
Pred. No.: 3.15e-63 Length: 1335
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13
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US-10-626-398-10 (1-389) x US-09-167-354-6 (1-1335)

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Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGGTCTTCGGCAGCTGGACCGCGTG-----CTGGCGGCGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCGTGGCCACGGTCTGGGCAACCGCGTGTGTATGCTCGCTTGTGGCCGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhe 62
Db 187 TCGAGCTCCGCCACCCAGACAACTTCTCTCTGCTCAACCTTCGCGCATCTCCGACTTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 247 GTCCGCGCCTTCTGCATCCCACTGTATGATACCTACCTACGTCGACAGCGCGCTGGACCTTC 306
Qy 82 GlyLysGlnAlaCysValPheTrpIleThrAspTyrLeuLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGGCGCTTCGACAGCTGTGGCTGGTAGTGAGTACCTGTGCTGTGACCTCTCTCTGCC 366
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## RESULT 9

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US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
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Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 367 TTCAACATGTGTCTATCAGCTACGACCGCTTCTCGTCCGTACCCGAGGGGTCTCATAC 426
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 427 CGSGCCACAGCGGTGACACGCGGGCGAGTGGCGAAGATGCTGTGGTGTGGTGCTG 486
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 487 GCCTTCTGTGTACGAGACGACCATCTG-----AGCTGGGAGTACCTGTCCGGG 537
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysIleTyrTrpPheAla 174
Db 538 GGAGCTTCATCCCGAGGGCCACTGCTATGCCGAGTTCTTCTACAACTGGTACTTCTCTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuValAlaTyrPheSerAla 194
Db 598 ATCAGCGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACTC 657
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 658 AGCATCTTACCTGAACATCCAGAGCGCACCCGCTCCGGCTCGATGGGCTCGAGAGGCA 717
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 718 GCCGGCCCCGAGCCCCCTCCGAGGGCCAGCCCTCACCCCCCAGCGCTGCTGTGG 777
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 778 GGCTGTGGCAGAAGGGCACGGGAGGCCATG-----CGCTGCACAGGTATGGG 828
Qy 236 -----AlaThrLeu----- 238
Db 829 GTGGTGAGGCGCGCTAGGCGCTGAGCGCGGGGAGCGACCCCTCGGGGTGCGGTGGG 888
Qy 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
Db 889 GGGGGTCTCGTGGCTTCAACCACTCCAGCTCCGGCAGCTCTCTCGAGGGGCATGAGAGG 948
Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 949 CCGGCG-----TCACCTCAAGAGGGGCTCCAAGCGCTCGGCGTCTCGGCTCGCTG 999
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1000 GAGAAGCGCATGAAGATGGTGTCCACAGAGCTTCACC-----CAGCGC 1041
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe 312
Db 1042 TTTGGGCTGTCTCGGACAGAAAGTGGCCAGTGGCTGCTGGCTCTGTGGGCAACTCGGCT 1101
Qy 313 AlaIleCystrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGGCTGTCTGGGCCCCCATACACGCTGTGATGATCATCGGGCGGCTGC---CATGGC 1158
Qy 333 AsnLeuThrLysSerThrTyrTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CACTCGCTCCCTGACTACTGTGTACGAAACCTCTCTGTGGCTCTGTGGGCAACTCGGCT 1218
Qy 353 ValAsnProPheLeuTyrProLeuCyHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGTCTCTACCTCTGTGTGCACACAGCTTCCGGCGGCTTTCACCAAGCTG 1278
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1279 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGC 1314
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[illegible]

## Alignment Scores:

Pred. No.: 3,15e-63 Length: 1335  
Score: 689.50 Matches: 161  
Percent Similarity: 53.5% Conservative: 70  
Best Local Similarity: 37.3% Mismatches: 132  
Query Match: 33.9% Indels: 69  
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-642-514-6 (1-1335)

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Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCGCGAGCGCTGGACCGCGTG-----CTGGCGCGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCGTGGCGACCGGTGCTGGCAACGCGCTGCTCATGCTCGCTTCGTCGCGGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCTTCGCGACCGCAGACACTTCTCTGCTCAACCTCGCATCTCGACTTCCTC 246
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr-----TyrTrpThrSer 81
Db 247 GTCGCGCTTCTGCATCCCACTGTATGTATGATACCTTACCTGCTGACAGCGCGCTGACCTTC 306
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrIleLeuCysThrAlaSerVal 101
Db 307 GCGCGCGCGCTCTGCAAGCTGTGGCTGGTAGTGAGTACCTGCTGTGCACCTCTCTCGCC 366
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 367 TTCAACATCGTGTCTATCAGCTACGACGCTCTCTGCTGCGTCCACCGAGCGGTCTCATAC 426
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 427 CGGCGCCAGCAGGCTGACACGCGCGCGCAGTGGGAAGATGCTGCTGTGGTGGTGTGCTG 486
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 487 GCCTTCTCTGCTGTACGACCGACCATCTCTG-----AGCTGGGAGTACCTGTCGCGG 537
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPheAla 174
Db 538 GGCAGCTCCATCCCGAGGCGCATGCTATGCCAGTTCCTCTACACTGGTACTTCTC 597
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 598 ATCAGCGCTTCCACCTGGAGTCTTTACGCCCTCTCTCAGCGTCACCTTCTTTAACCTC 657
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 658 AGCATCTACTCTGAATCCAGAGCGCACCGCTCCGGCTGGATGGGCTCGAGAGGCA 717
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 718 GCGCGCCCGAGCCCTCCCGAGCGCCAGCCCTCACACCCCGCCCTGGCTGGTGG 777
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 778 GGCTGCTGGCAGAGGGGCACGGGAGGCCATG-----CCGCTGCACAGGTATGGG 828
Qy 236 -----AlaThrLeu----- 238
Db 829 GTGGGTGAGCGCGCTAGGCGCTGAGCGCGGGAGCGACCTTCGGGGGTGGCGGTGGG 888
Qy 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
Db 889 GCGCGCTCCGTGGCTTCAACCATCTCCAGCTCCGCGCAGCTCTCTGAGGGGACATGAGAGG 948
Qy 253 SerArgArgLysSerSerLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 949 CCGCGC-----TCACTCAAGAGGGGCTCCAAGCGTCCGCGCTCTCTCGCGCTCGCTG 999
```

```
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1000 GAGAACGGCATGAAGATGGTGTCCAGAGCTTCACC-----CAGCGC 1041
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaPhe 312
Db 1042 TTTCCGGCTGTCTCGGACACAGAAAGTGGCAGCTCGTGGCCGCTCATCGTGCATCTTT 1101
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGCTCTGTGCGGCCCATACACGCTGCTGATCATCTCGGCCCGCTGC-----CATGGC 1158
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CATGGCTCCCTGACTACTGTTACGAAACCTCTCTGCTGCTGCTGGGCAACTCGGCT 1218
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCGCGCGGCTTTCACCAAGCTG 1278
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1279 CTCTGCCCGCAGAAAGCTCAAAATCCAGCCCCACAGC 1314
```

## RESULT 11

US-09-642-852-6  
; Sequence 6, Application US/09642852  
; Patent No. 6855560  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,852  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1335  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-852-6

Alignment Scores:  
Pred. No.: 3,15e-63 Length: 1335  
Score: 689.50 Matches: 161  
Percent Similarity: 53.5% Conservative: 70  
Best Local Similarity: 37.3% Mismatches: 132  
Query Match: 33.9% Indels: 69  
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-642-852-6 (1-1335)

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Qy 3 AlaAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 76 GCGCGCGCTTCGCGAGCGCTGGACCGCGTG-----CTGGCGCGCTCATGGCG 126
Qy 23 LeuLeuAlaIleAlaMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 127 CTGCTCATCGTGGCGACCGTCTGGGCAACGCGCTGCTCATGCTGCTGCTGCGCGGAC 186
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 187 TCGAGCTTCGCGACCGCAGAACTTCTCTGCTCAACCTCGCATCTCGACTTCCTC 246
```

```
Qy 63 ValGlyAlaIleAlaAlaProLeuThrLeuProSerSerLeuThr---TyrTrpThrSer 81
Db 247 GTGCGGCGCTTGTGATCCATCCCTGATGATGCTAGCTGCTGACAGCGCGCTGGACCTTC 306

Qy 82 GlyLysGlnAlaCysValPheTrpLeuLeuThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 307 GCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACACCTCTCTGCC 366

Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 367 TTCAACATCGTCTCATCAGCTACGACCGCTTCTCTGCTGCTGTCACCGAGCGGTCTCATAC 426

Qy 122 ArgAlaGlnHisSerGlyTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 427 CCGGCCACAGCGGTGACACCGCGCGGAGTGGCGGAGATGCTCTGCTGTGGTGGTGTG 486

Qy 142 SerPheMetThrAsnGlyProMetIleLeuLeuSerAspSerTrpGln----- 157
Db 487 GCCTTCTCTGTAGCGGACGACCATCTG-----AGCTGGAGTACCTGTGCGGG 537

Qy 158 ---AenSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpTyrPheAla 174
Db 538 GCGAGCTCATCCCGCGGCGCACCTGCTATGCCGAGTCTTCTTCAACACTGGTACTTCTC 597

Qy 175 LeuProThrSerLeuLeuGluPheLeuLeuProlleuLeuValAlaTyrPheSerAla 194
Db 598 ATCAGCGCTTCCACCTCGAGTCTTTTACGCCCTTCTCAGCGTCACCTCTTTAAACCTC 657

Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 658 AGCATCTACCTGACATCCAGAGGCGCACCGCTCCGCTGGATGGGGCTCGAGAGCA 717

Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 718 CCGCGCCCGAGCCCTCCCGAGCGCCAGCCCTCACCACCCACCGCTGGCTGTG 777

Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 778 GGCTGTGCGCAGAGGGGACCGGGAGGCCATG-----CCGCTGCACAGGTATGG 828

Qy 236 -----AlaThrLeu----- 238
Db 829 GTGGGTAGGCGCGCGTGTAGGCGCTGAGCGCGGGGAGCGACCTCGGGGTGGCGGTGG 888

Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 889 GCGGCTCGGTGCTTACCCACCTCCAGCTCCGCGACCTCTCGAGGGGCACTGAGAGG 948

Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 949 CCGGCG-----TCACCTCAAGAGGGGCTCCAGCGCTCGGGCTCTCGGCTCGCTG 999

Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnGlnArgGluHis 292
Db 1000 GAGAACCCATGAGATGGTGTCACAGAGCTTCACC-----CAGCGC 1041

Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe 312
Db 1042 TTTCGGCTGTCTCGGACAGGAAAGTGGCAAGTCTGCTGGCGCTCATGTGAGCATCTTT 1101

Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1102 GGGCTCTGCTGGGCGCCCATACACGCTGTGATGATCATCCGCGCGCGCTGC---CATGGC 1158

Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1159 CACTGCGCTCCTGACTACTGTGTACAAACCTCTCTGCGCTCTGTGGCGCAACTCGGCT 1218

Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1219 GTCAACCTGTCTCTACCTCTGTGCGCACACAGCTTCCGCGCGGCGCTTCCACAGCTG 1278

Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
```

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Db 1279 CTCTGCCCGCCAGAGCTCAAAATCCAGCCCGCCACAGC 1314

RESULT 12
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohca, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)....(1629)
US-09-891-053-21

Alignment Scores:
Pred. No.: 6,35e-63 Length: 2050
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13

US-10-626-398-10 (1-389) x US-09-891-053-21 (1-2050)

Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 346 GCGCGCGCTTCTCGGAGCGCTGACCGCGGTG-----CTGGCGCGCTCATGGCG 396

Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 397 CTGCTCATGTGGCGCAGGTGCTGGGCAACGCGGTGCTGCTCGCTTGTGGCCGAC 456

Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 457 TCGAGCGCTCGGCAACCCAGAACAACTTCTCTGCTCAACCTCGGCATCTCGGACTTCTC 516

Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 517 GTCGCGCGCTTCTGCATCCCATCTGATGATACCTTACCTGCTGACAGCGCGCTGACCTTC 576

Qy 82 GlyLysGlnAlaCysValPheTrpLeuLeuThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 577 GCGCGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACACCTCTCTGCC 636

Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 637 TTCAACATCGTCTCATCAGCTACGACCGCTTCTCTGCTGCTGCGGTACCGAGCGGTCTCATAC 696

Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
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Db 697 CGGGCCAGCAGGGGTGACACGCGGGCGAGTGGCGAAGATGCTGCTGTGGTGGTCTG 756
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 757 GCCTTCCTGCTGTACGGACCAACCATCTG-----AGCTGGAGTACCTTCGCGG 807
Qy 158 ---AenSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpPheAla 174
Db 808 GGCAGCTCCATCCCGAGGGCCATGCTATGCCAGTCTCTTCACTGGTACTTCTC 867
Qy 175 LeuProThrSerLeuLeuGluPheLeuLeuProIleLeuLeuValAlaTyrPheSerAla 194
Db 868 ATCAGCGCTTCCACCTGGAGTCTTTAGGCCCTTCTCTCAGCGTCACCTCTTTAACTC 927
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 928 AGCATCTACTGTGAATCATCCAGAGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGCA 987
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 988 GCCGGCCCGAGCCCTCCGAGGGCCAGCCCTCACACCCCCACCGCTGGCTGTGG 1047
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1048 GGCTGCTGGCAGAGGGGCACGGGGAGCCATG-----CGCTGCACAGTATGG 1098
Qy 236 -----AlaThrLeu----- 238
Db 1099 GTGGGTGAGCGCGGTAGCGCTCAGCGCCGGGAGCGACCTCGGGGGTGGCGTGGG 1158
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 1159 GCGCGCTCGGTGGCTTACCCACCTCCAGCTCCGCGAGCTCTCGAGGGGCATGAGAGG 1218
Qy 253 SerArgArgLysSerSerLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 1219 CCGGCG-----TCACTCAAGGGGCTCCAGCGCTCGGCTCGCTCGGCTCGCTG 1269
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnGlnArgGluHis 292
Db 1270 GAGAGCGCATGAAGTGTCTCCAGAGCTTCACC-----CAGCGC 1311
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPhe 312
Db 1312 TTTCGGCTGTCTCGGACAGAAAGTGGCCAACTCTTCTGCTCTCTGGCCCTCGCTCGCT 1371
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPheProGluArg 332
Db 1372 GGGCTCTGCTGGGCCCCATACCGCTGTGTATGATCATCCGGCGCGCTGC---CATGGC 1428
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1429 CACTGGCTCCCTGACTACTGTGTAGAAACCTCTCTTGGCTCTCTGGCCCACTCGGCT 1488
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuIleVal 372
Db 1489 GTCAACCTGTCTCTACCTCTGTGCCACACACAGCTTCGCGCGGGCTTCACCAAGCTG 1548
Qy 373 LeuProValArgArgGlnSerThrProHisAsn 384
Db 1549 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACACAGC 1584
```

## RESULT 13

```
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
```

```
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 9,76e-63 Length: 2665
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: 3 Gaps: 13
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US-10-626-398-10 (1-389) x US-09-949-016-5059 (1-2665)

```
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 367 GCGCGCGGCTTCTCGGCAGCTCGACCGCGGTG-----CTGGCGCGGCTCATGGCG 417
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 418 CTGCTCATCTGTCGACCGGTCTGGGCACCGCTGGTGTGCTCATGCTCGCTTCGTGGCGGAC 477
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 478 TCGAGCGCTCCGCCACCCAGAACAACTTCTCTCTCAACCTCGCATCTCCGATCTCTCTC 537
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 538 GTGCGCGCCTTCTGCATCCACCTGATGTATGATACCTACGTGCTGACAGCGCGCTGACCTTC 597
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 598 GCGCGCGGCGCTCTGCAAGCTGTGGCTGATGAGTACTACCTGTGTGTGTCACCTCTCTGCC 657
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 658 TTCAACATCTGCTCATCAGCTACGACCGCTTCTCTGTCGCTCACCCGAGCGGTCTCATAC 717
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 718 CCGGCCCGAGGGGTGACCGCGGGCGAGTGGCGGAAGATGCTGCTGGTGGGTGCTGCTG 777
Qy 142 SerPheMetThrAnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 778 GCCTTCCTGCTGTACGGACCGACCGCATCTG-----AGCTGGAGTACCTTCGCGGG 828
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpPheAla 174
Db 829 GGCAGCTCCATCCCGAGGGCCACTGCTATGCCAGTCTTCTTCAAACTGGTACTTCTC 888
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 889 ATCAGCGCTTCCACCTGGAGTCTTTAGCGCCCTCTCTCAGCGTCACTTCTTTAACTC 948
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 949 AGCATCTACTGTGAATCATCCAGAGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGCA 1008
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 1009 GCCGGCCCGAGCGCCCTCCGAGGGCCAGCCCTCACACCCCCACCGCTGGCTGTGG 1068
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
```



```
Db 1069 GCCTGCTGGCAGAGGGGACGGGGAGCCATG-----CCCTGCACAGGTATGGG 1119
Qy 236 -----AlaThrLeu----- 238
Db 1120 GTGGGTGAGCGCGCGCTAGCGCTGAGCGCGGGGAGCGACCTCGGGGGTGGCGGTGG 1179
Qy 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
Db 1180 GCGCGCTCGTGGCTTCCACCCACCTCCAGCTCCGGCAGCTCCCTCGAGGGGCGACTGAGAG 1239
Qy 253 SerArgArgLysSerSerLeuLeuProSerLeuAlaTyrLysAsnSerAsnValIle 272
Db 1240 CCGCGC-----TCACTCAAGAGGGGCTCCAAGCGCTCGCGCTCTCGGCCTCACTG 1290
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1291 GAGAAGCGCATGATGCTCCAGAGCTTCACC-----CAGCGC 1332
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaLaphe 312
Db 1333 TTTCGGCTGTCTCGGAGCAGGAAGTGGCAAGTCGCTGGCGCTCATCTGAGCATCTTT 1392
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1393 GGGCTCTGCTGGGCCCATACACGCTGTGATGATCATCCGGGGCGCGCTGC---CATGGC 1449
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1450 CACTGCGTCCCTGACTACTGTGTACGAACCTCTTCTGGCTCTGTGGCGCAACTCGGCT 1509
Qy 353 VallanProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1510 GTCAACCTCTGCTTACCTCTGTGTGCCACACACAGCTTCGCGGGGCGCTTCACCAAGCTG 1569
Qy 373 LeuProValArgGlnSerThrProHisAsn 384
Db 1570 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGC 1605
```

## RESULT 14

```
US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
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```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1
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## Alignment Scores:

Pred. No.:	9,91e-63	Length:	2689
Score:	689.50	Matches:	161
Percent Similarity:	53.5%	Conservative:	70
Best Local Similarity:	37.3%	Mismatches:	132
Query Match:	33.9%	Indels:	69
DB:	2	Gaps:	13

US-10-626-398-10 (1-389) x US-08-985-090-1 (1-2689)

```
Qy 3 AlaAsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSer 22
Db 366 GCGCGCGCTTCTCGGCAGCTGACCGCGGTG-----CTGGCCGCGCTCATGGCG 416
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 417 CTGCTCATCTGTCGGCACGCTGCTGGCAACGCTGTGTGTCATGCTGCGCTTCGTGGCCGAC 476
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 477 TCGAGCTTCCGACCCAGACACTTCTTCTGCTCAACCTCGCCATCTCGACTTCCTC 536
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 537 GTGCGGCGCTTCTGATCCATCTGATGTAACCTAGCTGACAGGCGCTGGACCTTC 596
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 597 GCGCGGGCGCTTCTGCAAGCTGTGGCTGTGTAGTGACCTACCTGTGTGACCTCTCTGCC 656
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 657 TTCAACATCGTGTCTCATGCTAGCACCGCTCTCTGTCGGTCACCGAGCGGTCTCATAC 716
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePhe 141
Db 717 CGGGCCCGCAGGCTGACACCGCGCGGCGCAGTCGGAGATGCTGTGTGTGGTGTGTG 776
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
Db 777 GCCTTCTGCTGTACGGACCAACCATCTCTG-----AGCTGGGAGTACCTGTGTCGGG 827
Qy 158 ---AsnSerThrThrGlu-----CysGluProGlyPheLeuLysLysTrpPheAla 174
Db 828 GGCAGCTCCATCCCGGAGGGCCACTGCTATGCCAGATTCTTCTACAACTGTGTACTCTC 887
Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 888 ATCAGCGCTTCCACCTGGAGTCTTTACGCGCTTCTCTCAGCGTCACCTCTTTAACCTC 947
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 948 AGCATCTACTGAATCCAGAGGCGCACCGCTCCGGCTGGATGGGGCTCGAGAGCA 1007
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 1008 GCGGCCCCGAGCCCCCTCCGAGGCGCAGCCCTCACACCCACCGCTGGTGGTGGTGG 1067
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1068 GGCTGCTGGCAGAGGGGCGACGGGAGGCCATG-----CCGCTGCACAGGTATGGG 1118
```

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Qy 236 -----AlaThrLeu----- 238
Db 1119 GTGGGTAGGCGCGCTAGGCGCTAGCGCGGAGGACCTTCGGGGTGGCGGTGGG 1178
Qy 239 -----ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLys 252
Db 1179 GCGCGCTCCGTGGCTTCACCCACCTCCAGCTCCGGCAGCTCTCGAGGGCAGTGAGAGG 1238
Qy 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValle 272
Db 1239 CCGGCG-----TCACCTACAGAGGGGCTCCAAAGCGCTCGGGCTCTCGGCCTCATG 1289
Qy 273 AlaSerLysMetGlyPheLeuSerHisSerAspSerLeuAlaLeuGlnArgGluHis 292
Db 1290 GAGAGCGCATGAGAGTGCTCCAGAGCTTCAC-----CAGCGC 1331
Qy 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaLysLeuAlaAlaPhe 312
Db 1332 TTTCGGCTGTCTCGGACAGGAAAGTGCCAAAGTCGCTGGCGCTCATCGTGAGCATCTTT 1391
Qy 313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db 1392 GGGCTGTGCTGGGCCCCATACACGCTGTGATGATCATCCGGCGCGCTGC---CATGGC 1448
Qy 333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db 1449 CACTGCGTCCCTGACTACTGTGTAGAAACCTCTCTGGCTCTCGGCGCGCTCGCT 1508
Qy 353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db 1509 GTCAACCTGTCTTACCTCTGTGCGCCACACAGCTTCGCGCGGCTTCACCAAGCTG 1568
Qy 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1569 CTCTGCCCCAGAAAGCTCAAAATCCAGCCCCACAGC 1604

RESULT 15
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; Sequence 1, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D. J. Goodearl and Sandra Gluckeman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
US-09-165-543-1

Alignment Scores:
Pred. No.: 9,91e-63 Length: 2689
Score: 689.50 Matches: 161
Percent Similarity: 53.5% Conservative: 70
Best Local Similarity: 37.3% Mismatches: 132
Query Match: 33.9% Indels: 69
DB: Gaps: 13

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Db 366 GCGCGCGGCTTCTCGGAGGCTGACCGCGGTG-----CTGGCGCGGCTCATGGCG 416
Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAsp 42
Db 417 CTGCTCATCTGCGCCACGGTGTGGCAACGCGTGTGTCATGCTGCGCTTCGTGGCGGAC 476
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 477 TCGAGCCTCGGCCACCCAGAAACAACTTCTCTGCTCAACCTCGCCATCTCCGACTTCCTC 536
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 537 GTGCGCGCCTTCTGCATCCCACTGTATGATCCCTACCTGCTGACAGCCCGCTGGACCTTC 596
Qy 82 GlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuLeuCysThrAlaSerVal 101
Db 597 GCGCGCGGCTCTGCAAGCTGTGGTAGTAGTACCTGTGCTGTGCTGCTGCTGCTGCTGCC 656
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 657 TTCACATCTGCTCATCATCAGTACGACCGCTTCTGTCGGTCTCCCGAGCGGTCTCATAC 716
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Db 717 CCGGCCCCAGCAGGTGTACACCGCGCGGCGAGTCGGAGATGCTGCTGGTGTGGGTGCTG 776
Qy 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln----- 157
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Qy 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrPheSerAla 194
Db 888 ATCAGCGCTTCCACCTGGAGTTCTTTACGCCCTTCTCTCAGCGTCACCTCTTTAACTTC 947
Qy 195 HisIleTyrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeu 210
Db 948 AGCATCTACCTGAACATCCAGAGCGCACCGCTCCGCTGGATGGGCTCGAGAGGCA 1007
Qy 211 SerHisProValLeuProSerAspSerSerSer----- 222
Db 1008 GCCGCGCCCGAGGCCCTCCGAGGCCACGCCCTCACACCCCGCTGGGTGTGTGG 1067
Qy 223 -----AspHisGlyHisSerCysArgGlnAspProAspSerArg----- 235
Db 1068 GGCTGCTGGCAGAGGGGCGACGGGAGGCCATG-----CGCTGCACAGGTATGGG 1118
Qy 236 -----AlaThrLeu----- 238
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Db 1119 GTGGGTGAGCGCGCTAGCGCTGAGCGCGGGAGGCGACCTCGGGGGTGGCGGTGGG 1178
QY 239 -----ProAlaArgLysGluThrAlaSerLeuGlySerAspLys 252
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QY 253 SerArgArgLysSerSerLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIle 272
Db 1239 CCGCGC-----TCACTCAAGAGGGGCTCAAGCCGTCGGCGTCTCGGCCCTCACYG 1289
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QY 293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaLaphe 312
Db 1332 TTTCGGCTGTCTCGGACACAGGAAGTGGCAAGTCGCTGGCGCTCATCGTGAGCATCTTT 1391
QY 313 AlaIleCysTipAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
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QY 333 AsnLeuThrLysSerThrTyrTyrHisThrAlaPheTyrLeuGlnTyrPheAsnSerPhe 352
Db 1449 CACTGGCTCCCTGACTACTGTGTACGAACCTCTCTGGCTCTGTGGCCCACTCGGCT 1508
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Db 1509 GTCAACCCCTGTCTTACCCCTGTGTCACCAACACAGCTTCGGCGGGCCCTTCACCAAGCTG 1568
QY 373 LeuProValArgArgGlnSerThrProProHisAsn 384
Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGC 1604
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Job time : 349 secs

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GenCore version 5.1.7  
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Run on: April 29, 2006, 23:57:38 ; Search time 3185 Seconds  
(without alignments)  
1009.981 Million cell updates/sec

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Perfect score: 2036

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Published Applications NA Main:

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10: /cgm2\_6/ptodata/1/pubpna/us11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	2025	99.5	1170 9	US-10-626-126-7 Sequence 7, Appli
3	2025	99.5	1170 9	US-10-626-398-7 Sequence 7, Appli
4	1308.5	64.3	1170 9	US-10-488-421-7 Sequence 7, Appli
5	1308.5	64.3	1173 3	US-09-812-216-1 Sequence 1, Appli
6	1308.5	64.3	1173 3	US-09-910-411-1 Sequence 1, Appli
7	1308.5	64.3	1173 3	US-09-875-076-13 Sequence 13, Appli

8	1308.5	64.3	1173 3	US-09-876-252-13 Sequence 13, Appli
9	1308.5	64.3	1173 5	US-10-052-193-1 Sequence 1, Appli
10	1308.5	64.3	1173 6	US-10-272-983-13 Sequence 13, Appli
11	1308.5	64.3	1173 6	US-10-354-769-1 Sequence 1, Appli
12	1308.5	64.3	1173 6	US-10-393-807-13 Sequence 13, Appli
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14	1308.5	64.3	1173 7	US-10-349-253A-1 Sequence 1, Appli
15	1308.5	64.3	1173 7	US-10-723-955-13 Sequence 13, Appli
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17	1308.5	64.3	1173 7	US-10-737-619-1 Sequence 1, Appli
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22	1308.5	64.3	1173 9	US-10-723-955-13 Sequence 13, Appli
23	1308.5	64.3	1266 3	US-09-891-138A-5 Sequence 5, Appli
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27	1308.5	64.3	3689 8	US-10-684-206-19 Sequence 19, Appli
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32	1244	61.1	1176 8	US-10-626-445-5 Sequence 5, Appli
33	1244	61.1	1176 9	US-10-626-136-5 Sequence 5, Appli
34	1244	61.1	1176 9	US-10-626-398-5 Sequence 5, Appli
35	1235.5	60.7	1176 8	US-10-626-445-6 Sequence 6, Appli
36	1235.5	60.7	1176 9	US-10-626-136-6 Sequence 6, Appli
37	1235.5	60.7	1176 9	US-10-626-398-6 Sequence 6, Appli
38	1166	57.3	1166 9	US-10-488-421-3 Sequence 3, Appli
39	1048.5	51.5	1103 9	US-10-488-421-1 Sequence 1, Appli
40	694.5	34.1	1239 3	US-09-891-053-2 Sequence 2, Appli
41	694.5	34.1	1239 8	US-10-759-463-2 Sequence 2, Appli
42	694.5	34.1	2700 3	US-09-891-053-5 Sequence 5, Appli
43	694.5	34.1	2700 8	US-10-759-463-5 Sequence 5, Appli
44	689.5	33.9	1335 3	US-09-350-206-3 Sequence 3, Appli
45	689.5	33.9	1335 3	US-09-349-755-3 Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-626-445-7  
; Sequence 7, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
US-10-626-445-7

Alignment Scores:  
Pred. No.: 4.67e-219 Length: 1170  
Score: 2025.00 Matches: 388  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 99.5% Indels: 0  
DB: 8 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-445-7 (1-1170)

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Db 1 ATGTGGCAATAAACAAGTACATCGCTTAACATCAATTAATAATTTCTTTGACATTTTAA 60

QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIle 40  
Db 61 ATGCTCTTACTAGCTATTGCTATATATGTTAGCAATGTCGGTCAATTTTAGCTTTTATT 120

QY 41 ValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAsp 60  
Db 121 GTGACAGAAATCTAGACATCGAAGTAATTTCTTTTCTTAACCTGGCCATTCGACAC 180

QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80  
Db 181 TTTCTTTGGTGGCAATTCGAATTCCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240

QY 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100  
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAGCATCT 300

QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120  
Db 301 GTGTATAATATTTGCTCATCAGTACCATCGTACCATGAGTCAATGCGGTGG 360

QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140  
Db 361 TATAGAGCTCAGCACTCTGGCACTCGGAATAATGCTACTCAGATGGTGGCTGTTGGATA 420

QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160  
Db 421 TTTCTCTTTCATGACAAATGGGCGGATGATTTCTGATTTTCTGACATCTGTGGCAATAGCACT 480

QY 161 ThrGluCysGluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeu 180  
Db 481 ACAGAAATGTGAACCTGGATTTTAAAGAGTGTACTTTGCTCTCCCTACATCATTTATG 540

QY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200  
Db 541 GAAATCTCTGATCCCATCTGTTAGTTGCTATTTTTCAGCGGCCATATTTTACTGGAGCCTG 600

QY 201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220  
Db 601 TGGAAAGCAGAGAAATCTGAGCAGGTGCTTCAGCCACCTGTACTCCCTCTGACTCTTCC 660

QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240  
Db 661 AGCAGTGACACCGAACCTCTTCGACAGACGAGACCCCGATTCAGGGGCGACTCTGCCAGCA 720

QY 241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260  
Db 721 CGGAAGAAACAACCTGCTCTCTTGGTTTCAGACAAGTCAGCGAGAAAGAGCAGTCTCTTG 780

QY 261 ProSerIleArgAlaTyrIlyAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280  
Db 781 TTTTCCATAAGAGCCTTACAGAAACAGCAATGTGATCGCTTCCAAATGGGCTTCTCTCC 840

QY 281 HisSerAspSerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLys 300  
Db 841 CACTCAGATTTCTGGCTCTTCAGCAAGGGAAACATATCGAACTTTTTCAGAGCCAGGAAA 900

QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTyrSer 320  
Db 901 TTAGCCAAAGTCACTGGCCCATCTCTTAGCAGCTTTTGGCCATTTGCGGCTCCATATTCA 960

QY 321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrIlySerSerThrTrpTrp 340  
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QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360  
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QY 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThr 380  
Db 1081 TGTCAACAAGCTTTTTCAGAGGCTTCTCTGAAATACTTCTCTGTGAGAGCAATCCACG 1140

QY 381 ProProHisAsnArgSerIleSerThr 389  
Db 1141 CCACCACACACCGCTCAATATCCACT 1167

RESULT 2  
US-10-626-126-7  
; Sequence 7, Application US/10626126  
; Publication No. US20050074770A1  
GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changliu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0033  
; CURRENT APPLICATION NUMBER: US/10/626,126  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Cavia porcellus  
US-10-626-126-7

Alignment Scores:  
Pred. No.: 4,67e-219 Length: 1170  
Score: 2025.00 Matches: 388  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 1  
Query Match: 99.5% Indels: 0  
DB: 9 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-126-7 (1-1170)

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Db 61 ATGCTCTTACTAGCTATTGCTATATATGTTAGCAATGTCGGTCAATTTTAGCTTTTATT 120

QY 41 ValAspArgAnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAsp 60  
Db 121 GTGACAGAAATCTTAGACATCGAAGTAATTTCTTTTCTTAACCTGGCCATTCGACAC 180

QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80  
Db 181 TTTCTTTGGTGGCAATTCGAATTCCTCTGTACATACCTTCTCGCTGACTTACTGGACT 240

QY 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100  
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCAATTAAGTACTATCTTTTATGTACAGCATCT 300

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Db 661 AGCAGTGACACCGGACACTCTCTGCAGACAGGACCCCGATTCAAGGGCGACTCTTCCAGCA 720
QY 241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
Db 721 CGGAAGAAACAACTCGCTCTTGGTTCAGCAAGTCAAGGAGAAAGAGCAGTCTCTTG 780
QY 261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280
Db 781 TTTTCCATAAGAGCCTACAGAAACAGCAATGTGTCGCTTCCAAATGGGCTTCTCTCC 840
QY 281 HisSerAspSerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLys 300
Db 841 CACTCAGATTCCTGGCTCTTCAGCAAGGAGGAAACATATCGAACTTTTCAGAGCCAGGAAA 900
QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCAAGTCTCTGGCCATCTCTTAGCAGCTTTTGCATTTGCTGGGCTCCATATTCA 960
QY 321 LeuThrThrValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyr 340
Db 961 CTGACTACAGTTATCTACTCATTTTCTTCTGAAAGGAACTTGACTTAATCAACCTGGTAC 1020
QY 341 HisThrAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeu 360
Db 1021 CATATCGCTTTTGGCTCCAGTGGTTCATTTCTCTTTGTAAATCCCTTTTGTATCCATTG 1080
QY 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThr 380
Db 1081 TGTCAAACGTTTTCAAGAGCTTCTCTGAAATACTTCTGTGGAAGGCAATCCACG 1140
QY 381 ProProHisAsnArgSerIleSerThr 399
Db 1141 CCACCACACACCGCTCAATATCCACT 1167
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## RESULT 3

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US-10-626-398-7
; Sequence 7, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Cavia porcellus
US-10-626-398-7
```

Alignment Scores:

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Pred. No.: 4,67e-219 Length: 1170
Score: 2025.00 Matches: 388
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-398-10 (1-389) x US-10-626-398-7 (1-1170)

QY 1 MetLeuAlaAsnAsnSerThrIleAlaLeuThrSerIleLysLeuSerLeuThrPheLeu 20
Db 1 ATGTGGCAATTAACAGTACCAATCGCTTAACATCAATATAAAATTTCTTTGACATTTTAA 60
QY 21 MetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIle 40
Db 61 ATGTCTTTTACTAGCTATTGCTATTAATGTAGGCAATGTCTGGTGCATTTTACTTTTATT 120
QY 41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAsp 60
Db 121 GTGACAGAAATCTTAGACATCGAAGTAATTAATCTTTTCTTAACCTGGCCATTCGACAC 180
QY 61 PhePheValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThr 80
Db 181 TTTCTTTGGGTGCAATTTGCAATTTCTCTGTACATACCTTCTCTGCTGACTTACTGGACT 240
QY 81 SerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSer 100
Db 241 TCTGAAAGCAAGCTTGTGTATTTTGGCTCATTAATCTGACTATCTTTTATGTACAGCATCT 300
QY 101 ValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrp 120
Db 301 GTGTATATATATGCTCTCATCAGCTACGATCGCTACCGAGTCACTCAATATGCCGTGTGG 360
QY 121 TyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIle 140
Db 361 TATAGAGCTCAGCACTCTGGCACCTGGAAATTTGCTACTCAGATGGTGGCTGTTGGATA 420
QY 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 421 TTTCTCTTTCATGACAAATATGGGCCGATGATTTCTGATTTTCAGACTCTCTGGCAGATAG 480
QY 161 ThrGluCysGluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeu 180
Db 481 ACAGATGTGAACCTGGATTTTAAAAAGTGGTACTTTGCTCTCCCTACATCATTTATG 540
QY 181 GluPheLeuIleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeu 200
Db 541 GAATTCCTGATCCCATCTTGTTAGTTGCTTAATTTTCAGCGCCCATATTTTACTGGAGCCTG 600
QY 201 TrpLysArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSer 220
Db 601 TGGAAAGCGAGAGAACTGAGCAGGTGCCTCAGCCACCTGTACTCTCCCTCTGACTCTTCC 660
QY 221 SerSerAspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAla 240
Db 661 AGCAGTGACACCGGACACTCTCTGCAGACAGGACCCCGATTCAAGGGCGACTCTTCCAGCA 720
QY 241 ArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeu 260
Db 721 CGGAAGAAACAACTCGCTCTTGGTTCAGCAAGTCAAGGAGAAAGAGCAGTCTCTTG 780
QY 261 ProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSer 280
Db 781 TTTTCCATAAGAGCCTACAGAAACAGCAATGTGTCGCTTCCAAATGGGCTTCTCTCC 840
QY 281 HisSerAspSerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLys 300
Db 841 CACTCAGATTCCTGGCTCTTCAGCAAGGAGGAAACATATCGAACTTTTCAGAGCCAGGAAA 900
QY 301 LeuAlaLysSerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSer 320
Db 901 TTAGCAAGTCTCTGGCCATCTCTTAGCAGCTTTTGCATTTGCTGGGCTCCATATTCA 960
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Qy 321 LeuThrThrValIleTyrSerPhePheProGluArgGlnLeuThrLysSerThrTyr 340  
Db 961 CTGACTACAGTTACTACTATTTTCTCTGAAAGGAACCTTGACTAAATCAACCTGGTAC 1020  
Qy 341 HisThrAlaPheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeu 360  
Db 1021 CATACTGCTTTTGGCTCCAGTGGTTCANATCCCTTTGTTAATCCCTTTTGTATCCATTG 1080  
Qy 361 CysHisLysArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThr 380  
Db 1081 TGTCAAAACGTTTTCAGAGGCTTTCTGAAATACTTCTGTGAGAGGCAATCCACG 1140  
Qy 381 ProHisAsnArgSerIleSerThr 389  
Db 1141 CCACACACACCGCTCAATATCCACT 1167

## RESULT 4

US-10-488-421-7  
; Sequence 7, Application US/10488421  
; Publication No. US20050239065A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc. [US/US]  
; APPLICANT: Gallagher, Michael J.  
; APPLICANT: Yates, Stephen L.  
; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES  
; FILE REFERENCE: 1367-13335W001  
; CURRENT FILING DATE: 2004-03-01  
; PRIOR APPLICATION NUMBER: US 60/316,762  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/332,697  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1170  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1170)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent  
; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Liou - Genbank Accession No. AF312230 - Liu et al., Mol.  
; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence  
; OTHER INFORMATION: only  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462  
; OTHER INFORMATION: are AAG and 988 is C  
US-10-488-421-7

## Alignment Scores:

Pred. No.: 1,17e-137 Length: 1170  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.5% Conservative: 48  
Best Local Similarity: 65.1% Mismatches: 84  
Query Match: 64.3% Indels: 3  
DB: Gaps: 9

US-10-626-398-10 (1-389) x US-10-488-421-7 (1-1170)  
Qy 5 AsnSerThrIleAlaLeuThr----SerIleLysIleSerLeuThrPheLeuMetSerLeu 23  
Db 13 AATAGCACAACTCAATTTATCACTAAGCACTCGTGTACTTTAGCATTTTATGTCTCTTA 72  
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43  
Db 73 GTAGCTTTTCTCTAATAATGCTAGGAATGCTTTGGTCATTTTAGCTTTTGGTGGACAA 132  
Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
Db 133 AACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGCCATCTCTGACTTCTTGTG 192  
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTyrThrSerGlyLys 83  
Db 193 GGTGTGATCTCCATTTCCATTTCTTGTATACCTCCCTCACACGCTGTCGAATGGGAAG 252  
Qy 84 GlnAlaCysValPheTyrLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103  
Db 253 GAAATCTGTGTATTTTGGCTCACTACTGACTATGATCGATCTCAATGCTGTGTCTTATAAC 312  
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrPyrArgAla 123  
Db 313 ATTGCTCTCATCAGCTATGATCGATCTGCTAGTCTCAATGCTGTGTCTTATAGAAT 372  
Qy 124 GlnHisSerGlyThrTyrPylsIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143  
Db 373 CAACATATGGGGTCTTGAAGATTGTACTCTGATGTTGGCCGTTTGGGTGCTCGCCTTC 432  
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTyrGlnAsnSerThrThrGluCys 163  
Db 433 TTAGTGAATGGGCAATGATTCTAGTTTCAGAGTCTTGGAGAGTGAAGTAGTGAATGT 492  
Qy 164 GluProGlyPheLeuLysLysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183  
Db 493 GAACCTGGATTTTTCGGAATGCTACATCCTGCCATCACATCATCTTCTGGAATCTGTG 552  
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTyrSerLeuTyrLysArg 203  
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATTGGAGCCTGTGGAAGCGT 612  
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223  
Db 613 GATCATCTCAGTAGTGCCAAAGCCATCCTCGACTGCTGCT---GTCCTCTCCACATC 669  
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243  
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCTATCGACAGAA 729  
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263  
Db 730 GTTCTGTCATCTTTCATTCAGAGACAGAGGAGAAAGAGTAGTCTCATGTTTTCCTCA 789  
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
Db 790 AGAACCAAGATGAATAGCAATACAAATTCCTTCCAAATGGGTCTCTTCTCCCATCAGAT 849  
Qy 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
Db 850 TCTGTAGTCTTTCACCAAGGGACATGTTGAACCTGCTTAGAGCCAGGAGATTAGCCAAG 909  
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTyrAlaProTyrSerLeuThrThr 323  
Db 910 TCACCTGGCCATCTCTTAGGGGTTTTCCTGCTGCTGCCATATATCTCTGTGTACA 969  
Qy 324 VallIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrThrHisThrAla 343  
Db 970 ATTGTCTTTCATTTTATTTTCTCCTCAGCAACAGGTCTCTAATCATGTTGGTATAGAATTGCA 1029  
Qy 344 PheTyrLeuGlnTyrPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363

Db 1030 TTTTGGCTTCAGTGGTTCAATCTCTTTGTCAATCTCTTTTGTATCCATGTTGTCAACAG 1089

Qy 364 ArgPheGlnIlyAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATATTTGTATAAAAGCAACCTCTACCATCACAA 1149

Qy 383 HisAsnArgSerIleSerThr 389

Db 1150 CACAGTCGGTCAGTATCTTCT 1170

# RESULT 5

US-09-812-216-1

; Sequence 1, Application US/09812216

; Patent No. US20020098539A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monsma, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/812,216

; PRIOR FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 09/414,010

; PRIOR FILING DATE: 1999-10-07

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-812-216-1

## Alignment Scores:

Pred. No.:	1,188-137	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.5%	Conservative:	48
Best Local Similarity:	65.1%	Mismatches:	84
Query Match:	64.3%	Indels:	3
DB:	3	Gaps:	3

US-10-626-398-10 (1-389) x US-09-812-216-1 (1-1173)

Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23

Db 13 AATAGCACATCAATTTATCACTAGCACTCGGTACTTTAGCATTTTATGTCCTTA 72

Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43

Db 73 GTAGCTTTGCTATAATGCTAGGAATGCTTTGGTCAITTTAGCTTTTGTGTGACAAA 132

Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63

Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTGCTCTTGTG 192

Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerLeuThrTyrTyrSerGlyLys 83

Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTACAGCTGTCGATGGATTTTGGAAAG 252

Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103

Db 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTATGACGATCTGTATATAAC 312

Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTrpArgAla 123

Db 313 ATTGTCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTCTTTATAGAACT 372

Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143

Db 373 CAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGGGTGTCGCCCTTC 432

Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrTrpGluCys 163

Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGTCTTGGAGAGTGAAGGTAGTGAATGT 492

Qy 164 GluProGlyPheLeuLysIleTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183

Db 493 GNACTGGATTTTTCGGAATGGTACATCTTCGCATCACATCATTTCTTGGAAATTCGTG 552

Qy 184 IleProIleLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203

Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATAATTTATTGGAGCTGTGGAAGCCT 612

Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223

Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCGACTGACTGCT--GTCTCTTCCCAATC 669

Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243

Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAGAGAGATCTCTTCTGCATCGACAGAA 729

Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263

Db 730 GTTCTGTCATCTCTTCAATTCAGAGAGACAGAGGAGAGAGTAGTCTCATGTCTTCTCA 789

Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283

Db 790 AGAACCAAGATGAATAGCAATCAATTCCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849

Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303

Db 850 TCTGTAGCTCTTCACCAAGGGAACATGTTGAATCTTAGAGCCAGAGATTAGCCAG 909

Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323

Db 910 TCAGTGGCCATCTCTTAGGGGTTTGTCTGTCTGTCTGCTCCATATCTCTGTTCACA 969

Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343

Db 970 ATTGTCTCTTCAATTTATTCCTCAGCAACAGGTCTCTAAATCAGTTTGTATAGAAATGCA 1029

Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363

Db 1030 TTTTGGCTTCAGTGGTTCATCTCTTGTCAATCTCTTTGTATTCATTTGTGTCAAG 1089

Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAGCAACCTCTACCATCACAA 1149

Qy 383 HisAsnArgSerIleSerThr 389

Db 1150 CACAGTCGGTCAGTATCTTCT 1170

## RESULT 6

US-09-910-411-1

; Sequence 1, Application US/09910411

; Patent No. US20020137054A1

; GENERAL INFORMATION:

; APPLICANT: Bergsma, Derk

; APPLICANT: Fitzgerald, Laura

; APPLICANT: Li, Xiatong

; APPLICANT: Michalovich, David

; APPLICANT: Zhu, Yuan

; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor

; FILE REFERENCE: GP70655-2C1

; CURRENT APPLICATION NUMBER: US/09/910,411

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: 09/693,761

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 09/497,790

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/431,898

; PRIOR FILING DATE: 1999-11-02

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:
Pred. No.: 118e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-910-411-1 (1-1173)

Qy 5 AenSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATGACCAATCAATTAATCAATGACACTCGTGTACTTTAGCATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTAATGCTAGGAATGCTTTGTCATTTAGCTTTGCTGGTGACAAA 132
Qy 44 AenLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTGACATCGAAGTAGTATTTTCTTAACCTTGCCATCTCTGACTTCTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTGCAATGGGATTTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
Db 253 GAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACGACATCTGTATATAC 312
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTrpArgAla 123
Db 313 ATTTGCTCATCAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
Db 373 CAACATACCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGTGTGGTGGTGGCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGTAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuGluPheLeu 183
Db 493 GAACTGGATTTTTCGGAATGGTATCATCTTTCGCAATCAGATCATCTTTCGAAATTCGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCACTTATGCTGCTTATTTCAACATGAATATTTATTTGAGGCTGTGGAGCGGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCGAAGCCATCTCTGACTGACTGCT---GTCTCTTCCAACTC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGGACACTCATTGAGAGTAGACTATCTTCAAGAGAGATCTTCTGTCATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTCTGCATCTCTTTCATTCAGAGACAGAGAGAGAGAGTAGTCTCATGTTTTCCTCA 789
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACATTTGCTTCCAAATATGGTTCCTTCTCCCAATCAGAT 849
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284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaAargLysLeuAlaLys 303
850 TCTGTAGCTCTTCCACAAAGGAAACATGTTGAAGCTGTTAGAGCCAGAGATTAGCCAG 909
304 SerLeuAlaIleLeuLeuAlaIlePheAlaIleCysTrpAlaProTyrSerLeuThr 323
910 TCACTGGCCATCTCTTTAGGGGTTTTGCTGTTTGTGCTGGCTCCATATCTCTGTTCA 969
324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTrpHisThrAla 343
970 ATTGTCTCTTCAATTTATTTCTCTCAGCAACAGGCTCTAAATCAGTTTGGTATAGAAATTGCA 1029
344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
1030 TTTTGGCTTCAGTGGTTCAATTTCTTTGTCAATCTCTTTGTATCCATTTGTGTGTCACAAG 1089
364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
1090 CGCTTTCAAAAGGCTTCTTGGAAATATTTTGTATATAAAAGCAACCTCTACCATCACA 1149
383 HisAsnArgSerIleSerThr 389
1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 7
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
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; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-875-076-13

Alignment Scores:
Pred. No.: 1.18e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-875-076-13 (1-1173)

QY 5 AasnSerThrIleAlaLeuThr----SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCACATCAATTTATCATCATGACCTCGGTACTTTTATGCTTTTATGCTCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAasnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTATATAGTAGGAATGCTTGGTCAATTTAGCTTTTGGTGGACAA 132
QY 44 AasnLeuArgHisArgSerAasnYrPhePheLeuAasnLeuAlaIleAlaPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCTGACTTCTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuYrIleProSerSerLeuThrYrTrpThrSerGlyLys 83
DB 193 GGTGTGATCTCCATCTCTTGTACATCCCTCACACGCTGTTCGAATGGGATTTTGGAAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAasnYrLeuLeuCysThrAlaSerValYrAasn 103
DB 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTATGACATCTGTATATAAC 312
QY 104 IleValLeuIleSerYrAspArgYrGlnSerValSerAasnAlaValTrpYrArgAla 123
DB 313 ATTGCTCTCATCAGCTATGATCGATACCTGTGCTCAATGCTGTGTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
DB 373 CAACATACCTGGGCTCTTGAAGATTGTACTCTGATGCTGGCCGCTTGGGTGCTGGCCTTC 432
QY 144 MetThrAasnGlyProMetIleLeuIleSerAasnYrTrpGlnAasnSerThrThrGluCys 163
DB 433 TTAGTGAATGGGCCAATGATCTTAGTCTTCAAGATCTTGGGAAGATGAAGGTAGTAATGT 492
QY 164 GluProGlyPheLeuLysYrTrpYrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
DB 493 GAACTGGATTTTTCGGAATGGTATACCTCTGGCCATCATCTTCTTGGNAATCGTG 552
QY 184 IleProIleLeuLeuValAlaYrPheSerAlaHisIleYrTrpSerLeuTrpLysArg 203
DB 553 ATCCAGTCACTCTTAGTCTGCTATTATTTCAACATGAATATTTATGGAGCCTGTGGAAGCT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAasnSerSerSerAasn 223
DB 613 GATCATCTCAGTAGGAGCCAAAGCCATCTCTGACTGACTGCT---GTCCTTCCCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAasnProAasnSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGGACATCTCAGAGGTAGACTATCTTCAAGAGAGATCTCTTCTGCTCGACAGAA 729
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QY 244 ThrThrAlaSerLeuGlySerAasnYrSerAasnYrSerAasnYrSerSerLeuLeuProSerIle 263
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QY 264 ArgAlaYrLysAasnSerAasnValIleAlaSerLysMetGlyPheLeuSerHisSerAasn 283
DB 790 AGAACCAAGATGAATAGCAATCAATTCCTTCCAAATGGGTCTTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
DB 850 TCTGTAGTCTTTCACCAAGGGAACATGTTGAACCTCTTAGAGCCAGGAGATTAGCCAAG 909
QY 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProYrSerLeuThrThr 323
DB 910 TCAGTGGCCATCTCTTGGGGTCTTGTGTCTGGGCTCCATATCTCTCTGTTCCACA 969
QY 324 ValIleYrSerPhePheProGluAasnLeuThrLysSerThrTrpYrHisThrAla 343
DB 970 ATTGCTCTTTCATTTTATTCCTCAGCAACAGGCTCTTAATCAGTTTGGTATAGAAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAasnSerPheValAasnProPheLeuYrProLeuCysHisLys 363
DB 1030 TTTTGGCTTCAGTGGTTCATTCCTTGTCAATCCTCTTGTATCCATTGTGTCAAG 1089
QY 364 ArgPheGlnYrAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
DB 1090 CGCTTTCAAAAGGCTTCTTGAAATATTTGTATAAAAGCAACCTCTACCATCACAA 1149
QY 383 HisAasnArgSerIleSerThr 389
DB 1150 CACAGTGGTCAGTATCTTCT 1170

RESULT 8
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
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/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-876-252-13

Alignment Scores:
Pred. No.: 1,18e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 3 Gaps: 3

US-10-626-398-10 (1-389) x US-09-876-252-13 (1-1173)

QY 5 AnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAAATCAATTTACTAGCACTCGGTGTACTTACCATTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAenValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCAATTTAGCTTTTGTGGACAAA 132
QY 44 AnLeuArgHisArgSerAenTyrPhePheLeuAenLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCTGACTTCTTTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTTCACACGCTGTTCGAATGGGATTTGGAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAen 103
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTATACAGCACTCTGTATATAAC 312
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QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaValTyrTrpArgAla 123
Db 313 ATTGTCCTCATCAGCTATGATGATCTGTCAGTCTCAATGCTGTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CACATACCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGCTTGGGTGTGGCCCTTC 432
QY 144 MetThrAenGlyProMetIleLeuIleSerAspSerTrpGlnAenSerThrTrpGluCys 163
Db 433 TTAGTGAATGGGCCAAATGATTTCTAGTTTTCAGAGTCTTGGAAAGGATGAGTGAATGT 492
QY 164 GluProGlyPheLeuLysTyrTrpPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGGATTTTTCGGAATGGTACATCTCTGCCATCACATCATCTTCTTGGAAATCTGTG 552
QY 184 IleProIleLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATTTGGAGCTGTGGAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
Db 613 GATCATCTCAGTAGGTGCCAAAGCCATCTCTGACTGCTGCT---GTCTCTTCCCAATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAGAGATCTCTTCTGTCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerSerLeuLeuProSerIle 263
Db 730 GTTCCTGCATCTCTTTCATTCAGAGACAGAGAGAGAGTAGTCTCATGTCTTCTCTCA 789
QY 264 ArgAlaTyrLysAenSerAenValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849
QY 284 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaAArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCACCAAGGAAACATGTTGAACTGCTTAGAGCCAGAGATTAGCCAA 909
QY 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
Db 910 TCACCTGGCCATCTCTTAGGGGTTTTTGTCTGTTCTGGGTCTCCATATCTCTGTTCACA 969
QY 324 ValIleTyrSerPhePheProGluArgAenLeuThrLysSerThrTrpTrpHisThrAla 343
Db 970 ATTGTCTTTCATTTTATTTCTCTCAGCAACAGGTCTCTAAATCAGTTTGGTATAGAATTGCA 1029
QY 344 PheTrpLeuGlnTrpPheAenSerPheValAenProPheLeuTyrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTATCCATTTGTGTCAAG 1089
QY 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTCTTGAATAATTTTGTATAAAAAGCAACCTCTACCATCACAA 1149
QY 383 HisAenArgSerIleSerThr 389
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 9
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Alignment Scores:
Pred. No.: 118e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 5 Gaps: 3

US-10-626-398-10 (1-389) x US-10-052-193-1 (1-1173)

QY 5 AnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
DB 13 AATAGCAGATCATATTAATCATAGCACTCGTGTTACTTTTAGCAATTTTATGTCCTTA 72
QY 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
DB 73 GTAGCTTTTGCTATAATGCTAGAAATGCTTTGGTCAITTTAGCTTTTGTGTGCAAA 132
QY 44 AnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
DB 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGCCCATCTCTGACTTCTTTGTG 192
QY 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
DB 193 GGTGTGATCTCCATTCCTTTGACATCCCTCACGCTGTTTGAATGGGATTTTGAAG 252
QY 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
DB 253 GAAATCTGTATTTTGGCTCACTACTGATCTATCTGTTATGTACAGCATCTGTATATAC 312
QY 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTrpArgAla 123
DB 313 ATTGCTCTCATCAGCTATGATCGATACCTGTCTCAATGCTGTCTTATAGAACT 372
QY 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143
DB 373 CAACATCTGGGCTTCAAGATTTTACTCTGATGGTGGCGTGTGGTGTGCGCTTC 432
QY 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
DB 433 TTAGTGAATGGCCATGATTTCTAGTTTCAGATCTTGGAGGATGAAGTAGTGAATGT 492
QY 164 GluProGlyPheLeuLysIleTyrTrpPheAlaLeuProThrSerSerLeuGluPheLeu 183
DB 493 GAACCTGATTTTTCGGAATGGTACATCTCTTGCATCACATCATCTTCTTGAATTCGTG 552
QY 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
DB 553 ATCCAGTCATCTTAGTGTGCTTATTTCAACATGAATATTTATTTGAGGCTCTGGAAGCGT 612
QY 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
DB 613 GATCATCTCAGTAGTGTCAAGCCATCTCTGACTGACTGTCT---GTCTCTTCAACATC 669
QY 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
DB 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGTCATCGACAGAA 729
QY 244 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle 263
DB 730 GTTCCTGTCATCTTTCATTTCAAGAGACAGAGAGAAAGAGTAGTCTCATGTTTCTCTCA 789
QY 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
DB 790 AGAACCAAGATGAATAGCATACATTCCTTCCAAATGGGTTCCTCTCCCAATCAGAT 849

; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Alignment Scores:
Pred. No.: 118e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3

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DB: 6 Gaps: 3
US-10-626-398-10 (1-389) x US-10-272-983-13 (1-1173)
Qy 5 AnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAAAATCAATTTATCTAAGCACTCGTGTTACTTTAGCATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTAATAAGCTAGGAATGCTTTGGTCATTTTAGCTTTTGTGTGGACAA 132
Qy 44 AnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCTGACTCTCTTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTATCCCTCACAGCTGTTCGAATGGATTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCysThrAlaSerValTyrrAsn 103
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312
Qy 104 IleValLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrArgAla 123
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Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAAATGGCCAAATGATTTCTAGTTTCAGAGCTTCGGAAGGATGAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysIleTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGATTTTTCGGAATGGTATCATCTTGCATCATCATCTTCTTGGAAATTCGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTroSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGATATTTATTTGGAGCTGTGGAAAGCT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGTGGCCAAAGCATCTCTGGACTGACTGCT---GTCTCTTCCAAATC 669
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Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTGTCATCTTTTCATTCAGAGACAGAGGAGAAAGAGTAGTCTCATGTTTTCCTCA 789
Qy 264 ArgAlaTyrrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATCATAGCATATACATATGCTTCCAAATGGGTCTCTTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCCACAAAGGAAACATGTTGAACCTGTAGAGCCAGGAGATTAGCCAA 909
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrrSerLeuThrThr 323
Db 910 TCACATGGCCATCTCTTGGGGGTTTGTGTGTGTGCTGGGCTCCATATCTCTGTTCACA 969
Qy 324 ValIleTyrrSerPheProGluArgAsnLeuThrLysSerThrTrpTyrrHisThrAla 343
Db 970 ATGTGCTTTTCATTTTATCTTCAGCAACAGGCTCTTAATCAGTTTGGTATAGAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrrProLeuCysHisLys 363
Db 1030 TTTTGGCTTCAGTGGTTCATTTCTTTGTCAATCTCTTTTGTATCCATTTGTGTCAAG 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgGlnSerThrPro---Pro 382
Db 1090 CGCTTTCAAAGGCTTTCTTTGAAAATATTTTGTATAAAAAGCAACCTCTACCATCAAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
Db 1150 CACATCGGTGAGTATCTTCT 1170
RESULT 11
US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter. Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: GB 9925641.4
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: GB 0009973.9
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-769-1
Alignment Scores:
Pred. No.: 118e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: 6 Gaps: 3
US-10-626-398-10 (1-389) x US-10-354-769-1 (1-1173)
Qy 5 AnSerThrIleAlaLeuThr--SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCAAAATCAATTTATCTAAGCACTCGTGTTACTTTTAGCATTTTATGTCCTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
Db 73 GTAGCTTTGCTAATAAGCTAGGAATGCTTTGGTCATTTTAGCTTTTGTGTGGACAA 132
Qy 44 AnLeuArgHisArgSerAsnTyrrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63
Db 133 AACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCTGACTCTCTTTGTG 192
Qy 64 GlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThrTyrrTrpThrSerGlyLys 83
Db 193 GGTGTGATCTCCATTCCTTTGTATCCCTCACAGCTGTTCGAATGGATTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrrLeuLeuCysThrAlaSerValTyrrAsn 103
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312
Qy 104 IleValLeuIleSerTyrrAspArgTyrrGlnSerValSerAsnAlaValTrpTyrrArgAla 123
Db 313 ATTGTCTCATCAGCTATGATGATACCTGTCAGTCTCAATGCTGTGTCTTATAGAAGT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
Db 373 CAACATATGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGGGTCTGCGCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
Db 433 TTAGTGAAATGGCCAAATGATTTCTAGTTTCAGAGCTTCGGAAGGATGAGTGAATGT 492
Qy 164 GluProGlyPheLeuLysIleTyrrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
Db 493 GAACCTGATTTTTCGGAATGGTATCATCTTGCATCATCATCTTCTTGGAAATTCGTG 552
Qy 184 IleProIleLeuLeuValAlaTyrrPheSerAlaHisIleTyrrTroSerLeuTrpLysArg 203
Db 553 ATCCAGTCATCTTAGTCGCTTATTTCAACATGATATTTATTTGGAGCTGTGGAAAGCT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp 223
Db 613 GATCATCTCAGTAGTGGCCAAAGCATCTCTGGACTGACTGCT---GTCTCTTCCAAATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGTCATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
Db 730 GTTCTGTCATCTTTTCATTCAGAGACAGAGGAGAAAGAGTAGTCTCATGTTTTCCTCA 789
Qy 264 ArgAlaTyrrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
Db 790 AGAACCAAGATCATAGCATATACATATGCTTCCAAATGGGTCTCTTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
Db 850 TCTGTAGCTCTTCCACAAAGGAAACATGTTGAACCTGTAGAGCCAGGAGATTAGCCAA 909
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrrSerLeuThrThr 323
Db 910 TCACATGGCCATCTCTTGGGGGTTTGTGTGTGTGCTGGGCTCCATATCTCTGTTCACA 969
Qy 324 ValIleTyrrSerPheProGluArgAsnLeuThrLysSerThrTrpTyrrHisThrAla 343
Db 970 ATGTGCTTTTCATTTTATCTTCAGCAACAGGCTCTTAATCAGTTTGGTATAGAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrrProLeuCysHisLys 363
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Db 553 ATCCAGCATCTTAGTCGCTTAATTTCAACATGAAATATTTATTGGAGCCTGTGGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
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Db 613 GATCATCTCAGTAGGTGCAAGCCATCTCGACTGACTGCT--GTCTCTTCCAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
   :::::::::::::::::::::::::::::
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTTTCGCATCGACAGNA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
   :::::::::::::::::::::::::::::
Db 730 GTTCTCGCATCTCTTCATTCAGAGACAGACAGAGAGAGAGTAGTCTCATGTTTCTCA 789
Qy 264 ArgAlaThrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283
   :::::::::::::::::::::::::::::
Db 790 AGAACCAAGATGATAGCAATACAAATGCTTCCAAAATGGGTCTCTTCTCCCAATCAGAT 849
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303
   :::::::::::::::::::::::::::::
Db 850 TCTGTAGCTCTTCAACCAAGGGAACATGTTGAAGTCTTAGAGCCAGGAGATTAGCCAA 909
Qy 304 SerLeuAlaLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323
   :::::::::::::::::::::::::::::
Db 910 TCATGGGCATCTCTTAGGGTCTTCTGTTGCTGGCTCCATATCTCTGTTTCA 969
Qy 324 VallIeTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343
   :::::::::::::::::::::::::::::
Db 970 ATTGTCCTTCAATTTATTTCTCAGCAACAGGTCTCTAAATCAGTTGGTAGAATTGCA 1029
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363
   :::::::::::::::::::::::::::::
Db 1030 TTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTATCCATTGGTGCACAA 1089
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382
   :::::::::::::::::::::::::::::
Db 1090 CGCTTTCAAGAGCTTTCTGAAATATTTTGTATAAAAGCAACCTCTACCACAA 1149
Qy 383 HisAsnArgSerIleSerThr 389
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Db 1150 CACAGTCGGTCAGTATCTTCT 1170

RESULT 13
US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.COM
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-820A-13

Alignment Scores:
Pred. No.: 1,18e-137 Length: 1173
Score: 1308.50 Matches: 252
Percent Similarity: 77.5% Conservative: 48
Best Local Similarity: 65.1% Mismatches: 84
Query Match: 64.3% Indels: 3
DB: Gaps: 3

US-10-626-398-10 (1-389) x US-10-417-820A-13 (1-1173)
Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db 13 AATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTTAGCATTTTATGTCTTTA 72
Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43
   :::::::::::::::::::::::::::::
Db 73 GTAGCTTTTGTCTAATAATGCTAGGAAATGCTTTGGTCATTTTGTGTTGGACAAA 132
Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePheVal 63
   :::::::::::::::::::::::::::::
Db 133 AACCTTAGACATCGAAGTAGTTATTTTTTTTCTTAACCTTGGCCATCTCTGACTTCTTGT 192
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83
   :::::::::::::::::::::::::::::
Db 193 GGTGTGATCTCCATTTCCITTTGTACATCCTCACACGCTGTTTCAATGGATTTTGGAAAG 252
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103
   :::::::::::::::::::::::::::::
Db 253 GAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCATCTGTATATAAC 312
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123
   :::::::::::::::::::::::::::::
Db 313 ATTGTCTCATCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143
   :::::::::::::::::::::::::::::
Db 373 CAACATACCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTGGTGGTGGCTTC 432
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163
   :::::::::::::::::::::::::::::
Db 433 TTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGAGTGAAGAGTGTAGTGT 492
Qy 164 GluProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183
   :::::::::::::::::::::::::::::
Db 493 GAACTTGAATTTTTCGGAATGGTACATCTCTGATCATCATCATCATCTTGGAAATTCGT 552
Qy 184 IleProIleLeuLeuValAlaThrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203
   :::::::::::::::::::::::::::::
Db 553 ATCCCATGATCTTAGTCGCTTATTTCAACATGAAATATTTATGGAGCCTGTGGAAGCGT 612
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223
   :::::::::::::::::::::::::::::
Db 613 GATCATCTCAGTAGGTGCAAGCCATCTCGACTGACTGCT--GTCTCTTCCAACATC 669
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243
   :::::::::::::::::::::::::::::
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTCGATCGACAGAA 729
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263
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Db 730 GTTCTGCACTCTTTTCATTTACAGAGACAGAGAGAGTAGTCTCATGTTTCTCTCA 789  
 Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
 Db 790 AGAACCAAGATGATGACCAATACAAATGCTTCCAAATGGGTCTCTCTCCCAATCAGAT 849  
 Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
 Db 850 TCTGTAGCTCTTCACCAAGGAGACATGTGAACTGCTTAGAGCCAGAGATAGCCAG 909  
 Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323  
 Db 910 TCATCGGCCATCTCTTAGGGGTTTTGCTGTGGCTCCCATATCTCTGTTCACA 969  
 Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343  
 Db 970 ATTTGCTCTTTCAATTTTCTCTCAGCAACAGGCTCTAAATCAGTTTGGTATAGAAATGCA 1029  
 Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363  
 Db 1030 TTTTGGCTTCAGTGGTTCAATCTCTTTGTCAATCTCTTTTGTATCCATTTGTGCACAG 1089  
 Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382  
 Db 1090 CGCTTTCAAGAGCTCTCTTGAATATATTTTGTATAAAAAAGCAACCTCTACCATCACAA 1149  
 Qy 383 HisAsnArgSerIleSerThr 389  
 Db 1150 CACAGTCGGTCAGTATCTTCT 1170

## RESULT 14

## US-10-349-253A-1

; Sequence 1, Application US/10349253A  
 ; Publication No. US20040043393A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aubart, Kelly  
 ; APPLICANT: Bergsma, Derek  
 ; APPLICANT: Fitzgerald, Laura  
 ; APPLICANT: Graybill, Todd  
 ; APPLICANT: Li, Xiatong  
 ; APPLICANT: Michalovich, David  
 ; APPLICANT: Morrow, Dwight  
 ; APPLICANT: Zhu, Yuan  
 ; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor  
 ; FILE REFERENCE: GP70655-2C2  
 ; CURRENT APPLICATION NUMBER: US/10/349,253A  
 ; CURRENT FILING DATE: 2003-01-21  
 ; PRIOR APPLICATION NUMBER: 09/910,411  
 ; PRIOR FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: 09/693,761  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 09/497,790  
 ; PRIOR FILING DATE: 2000-02-03  
 ; PRIOR APPLICATION NUMBER: 09/431,898  
 ; PRIOR FILING DATE: 1999-11-02  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1173  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-349-253A-1

## Alignment Scores:

Pred. No.:	1,18e-137	Length:	1173
Score:	1308.50	Matches:	252
Percent Similarity:	77.5%	Conservative:	48
Best Local Similarity:	65.1%	Mismatches:	84
Query Match:	64.3%	Indels:	3
DB:	7	Gaps:	3

US-10-626-398-10 (1-389) x US-10-349-253A-1 (1-1173)

Qy 5 AsnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23  
 Db 13 AATACACAACTCAATTTATCACTAAGACTCTGGTACTTTTACCATTTTATGTCCTTA 72  
 Qy 24 LeuAlaIleAlaIleMetLeuGlyAsnValValIleLeuAlaPheIleValAspArg 43  
 Db 73 GTAGCTTTTGTCTATATGCTAGGAAATGCTTTGGTCACTTTTACGCTTTTGTGGGACAA 132  
 Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
 Db 133 AACCTTAGACATCGAAGTAGTTATTTTCTTAACTTTGGCCATCTCTGACTTCTTTGTG 192  
 Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTrpThrSerGlyLys 83  
 Db 193 GGTGTGATCTCCATTCCTTTGACATCCCTCACAGCTGTTCCGAAATGGGATTTTGGAAAG 252  
 Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103  
 Db 253 GAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTATACAGCATCTGTATATAAC 312  
 Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAla 123  
 Db 313 ATTTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTGTCTTATGAAC 372  
 Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTrpIlePheSerPhe 143  
 Db 373 CAACATCTGGGCTCTTGAAGATTCTTACTCTGATGGTGGCCGTTTGGGTGGCCCTTC 432  
 Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163  
 Db 433 TTAGTGAATGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAAGTAGTGAATGT 492  
 Qy 164 GluProGlyPheLeuLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183  
 Db 493 GAACCTGGATTTTTCGGAATGGTACATCTTTCGCATCACATCATCTCTTGGAAATTCGTG 552  
 Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203  
 Db 553 ATCCCAAGTCATCTTAGTCGCTTATTTCAACATGAATATTTATGGAGCTGTGGAAAGCGT 612  
 Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223  
 Db 613 GATCATCTCAGTAGTGGTCCAAAGCCATCTTGGAGTACGTCT---GTCTCTTCCAAATC 669  
 Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243  
 Db 670 TGTGACACTCATTCAGAGGTAGACTATCTTCCAGGAGATCTCTTTCGCATCGACAGAA 729  
 Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSerIle 263  
 Db 730 GTTCTGTCATCTTTCATTTCAGAGAGACAGAGGAGAAAGAGTAGTCTCATGTTTCTCTCA 789  
 Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
 Db 790 AGAACCAAGATCAATAGCAATACAAATGCTTCCAAATGGGTCTCTTCTCCCAATCAGAT 849  
 Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
 Db 850 TCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGTAGAGCCAGAGATAGGACCAAG 909  
 Qy 304 SerLeuAlaIleLeuLeuAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323  
 Db 910 TCATCGGCCATTTCTTAGGGGTTTTTGTCTTGGCTGCCATATTTCTCTGTTCACA 969  
 Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThrAla 343  
 Db 970 ATTTGCTTTTCAATTTTATCTCTCAGCAACAGGCTCTTAATCAGTTTGGTATAGAAATGCA 1029  
 Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363  
 Db 1030 TTTTGGCTTCAGTGGTTCAATCTCTTTGTCAATCTCTTTTGTATCCATTTGTGTACAAAG 1089  
 Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382

Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAACCTCTACCATCACAA 1149  
Qy 383 HisAsnArgSerIleSerThr 389  
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

## RESULT 15

US-10-723-955-13  
; Sequence 13, Application US/10723955  
; Publication No. US20040110238A1  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lehman-Bruinsma, Karin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Gore, Martin  
; APPLICANT: White, Carol  
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: 7.0S29.CON  
; CURRENT APPLICATION NUMBER: US/10/723,955  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 10/417,820  
; PRIOR FILING DATE: 2003-4-16  
; PRIOR APPLICATION NUMBER: 09/416,760  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: 60/110,060  
; PRIOR FILING DATE: 1998-11-27  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,852  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/123,944  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,945  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,948  
; PRIOR FILING DATE: 1999-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-955-13

Alignment Scores:  
Pred. No.: 1,188-137 Length: 1173  
Score: 1308.50 Matches: 252  
Percent Similarity: 77.5% Conservative: 48  
Best Local Similarity: 65.1% Mismatches: 84  
Query Match: 64.3% Indels: 3  
DB: 7 Gaps: 3

US-10-626-398-10 (1-389) x US-10-723-955-13 (1-1173)

Qy 5 AnSerThrIleAlaLeuThr---SerIleLysIleSerLeuThrPheLeuMetSerLeu 23  
Db 13 AATAGCACAAATCAATTTTACCTACGACGCTGTTACTTTTATGACATTTTATGCTCTTA 72  
Qy 24 LeuAlaIleAlaIleMetLeuGlyAnValValIleLeuAlaPheIleValAspArg 43  
Db 73 GTAGCTTTTGCTATATGCTAGGAATGCTTTGGTCATTTTACCTTTTGTGGTGGACAA 132

Qy 44 AsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPheVal 63  
Db 133 AACCTTAGACATCGAATAGTATTATTTTCTTAACCTGGCCATCTCTGACTTCTTTGTG 192  
Qy 64 GlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThrTyrTyrTrpThrSerGlyLys 83  
Db 193 GGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTCGAATGGGATTTTGGAAAG 252  
Qy 84 GlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsn 103  
Db 253 GAAATCTGTGTATTTTGGCTCACTACTACTATCTGTATGTACAGCATCTGTATATAAC 312  
Qy 104 IleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTyrTrpTrpArgAla 123  
Db 313 ATTGTCTCATCAGCATGATGATCGATACCTGTGAGTCTCAAAATGCTGTGTCTTATAGAACT 372  
Qy 124 GlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaValTyrIlePheSerPhe 143  
Db 373 CAACATAGTGGGTCTTGAAGATTGTACTCTGATGGTGGCGTTTGGGTGCTGGCCCTTC 432  
Qy 144 MetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThrThrGluCys 163  
Db 433 TTAGTGAATGGGCCAATGATTCTAGTTTTCAGAGTCTTGGAAAGGATGAGGTAGTGAATGT 492  
Qy 164 GluProGlyPheLeuLysLysTyrTyrPheAlaLeuProThrSerLeuLeuGluPheLeu 183  
Db 493 GAACCTGGATTTTTTTCGGAATGATGATACATCTTCCCATCATCATTTCTTGGAAATTCGTG 552  
Qy 184 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg 203  
Db 553 ATCCAGTCACTTAGTCGCTTATTTCAACATGAATATTATTGGAGCTGTGGAAGCGT 612  
Qy 204 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSerAsp 223  
Db 613 GATCATCTCAGTAGTGGCCAAAGCCATCTCTGAGTCTGCTCTTCTTCCCAATC 669  
Qy 224 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu 243  
Db 670 TGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTCTGCAATCGACAGA 729  
Qy 244 ThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerSerLeuLeuProSerIle 263  
Db 730 GTTCTGCTATCTTTCATTCAGAGAGACAGAGAGAGAGATGCTCATGTCTTCTTCCCTCA 789  
Qy 264 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp 283  
Db 790 AGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTCTCTTCTCCCAATCAGAT 849  
Qy 284 SerLeuAlaLeuGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys 303  
Db 850 TCTGTAGCTCTTCACAAAGGGAACATGTTGAACCTGCTTAGAGCCAGAGATAGCCAAAG 909  
Qy 304 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThr 323  
Db 910 TCATGGCCATCTCTTAGGGGTTTTCGTTGCTGGTCTGGCTCCATATTTCTGTCTTCA 969  
Qy 324 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTyrTrpThrHisThrAla 343  
Db 970 ATTGTCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTTTGGTATAGAAATGCA 1029  
Qy 344 PheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys 363  
Db 1030 TTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTATTCATTTGTGTACAG 1089  
Qy 364 ArgPheGlnLysAlaPheLeuLysIleLeuProValArgArgGlnSerThrPro---Pro 382  
Db 1090 CGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAACCTCTACCATCACAA 1149  
Qy 383 HisAsnArgSerIleSerThr 389  
Db 1150 CACAGTCGGTCAGTATCTTCT 1170

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Job time : 3206 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 29, 2006, 23:57:49 ; Search time 570 Seconds

(without alignments)  
2771.638 Million cell updates/sec

Title: US-10-626-398-10

Perfect score: 2036

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DLOCAL=200 -THR SCORE=pct -THR MAX=100  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

Published Applications NA.New:\*\*

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12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
15: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	681.5	33.5	2761	11	US-11-036-196-2003
2	681.5	33.5	2814	14	US-11-136-527-3990

3	620.5	30.5	2824	14	US-11-136-527-127
4	549	27.0	1326	14	US-11-241-956-19
5	409.5	20.1	2348	14	US-11-136-527-3691
6	407.5	20.0	4095	14	US-11-136-527-2030
7	404.5	19.9	3578	11	US-11-036-196-1495
8	403.5	19.8	1773	14	US-11-127-877-17
9	403.5	19.8	1974	14	US-11-124-368A-14
10	402.5	19.8	2733	14	US-11-136-527-2435
11	397	19.5	2699	14	US-11-127-877-5
12	392	19.3	2633	14	US-11-136-527-3114
13	389	19.1	3741	14	US-11-136-527-751
14	387	19.0	1862	14	US-11-136-527-2377
15	385.5	18.9	2089	14	US-11-127-877-13
16	385.5	18.9	2290	14	US-11-127-877-13
17	378	18.6	8590	11	US-11-114-798-46
18	378	18.6	197241	11	US-11-114-798-47
19	376.5	18.5	2089	14	US-11-128-061-892
20	376.5	18.5	2089	14	US-11-128-049-892
21	373	18.3	1401	14	US-11-127-877-4
22	370	18.2	1203	9	US-10-499-210-1
23	370	18.2	1860	14	US-11-136-527-2642
24	364	17.9	4061	14	US-11-136-527-2806
25	360	17.7	2483	14	US-11-136-527-2847
26	359.5	17.7	2591	14	US-11-136-527-1944
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29	356	17.5	2509	14	US-11-136-527-3738
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33	343	16.8	6501	14	US-11-136-527-3427
34	338	16.6	1374	11	US-11-232-805-42
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36	338	16.6	1443	8	US-10-521-162-41
37	337	16.6	2809	14	US-11-136-527-2036
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39	332.5	16.3	3893	14	US-11-136-527-2295
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#### ALIGNMENTS

RESULT 1  
US-11-036-196-2003  
; Sequence 2003, Application US/11036196  
; Publication No. US20060078900A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgin, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/11/036,196  
; CURRENT FILING DATE: 2005-01-18  
; PRIOR APPLICATION NUMBER: US/10/152,319  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807





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US-10-626-398-10 (1-389) x US-11-136-527-3990 (1-2814)
QY 3 AlaAenAenSerThrIleAlaLeuThrSerIleLysLeuThrPheLeuMetSer 22
Db 403 GCGCGGGCTTCTCGCTCGCTGGACCGGTGC-----CTGGCTCGCTCATGGCG 453
QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAenValValIleAlaIleAlaPheLeuValAap 42
Db 454 CTGCTCATGTCGCGCCACAGTACTGGGCAACGGCTGTCATGCTCGCCCTCGTGGCGGAT 513
QY 43 ArgAenLeuArgHisArgSerAenTyrrPhePheLeuAenLeuAlaIleAlaAapPhePhe 62
Db 514 TCGAGGCTCGGCACCGACCAACTTCTTCTGCTCAACTCGGCATCTCCGACTTCCTC 573
QY 63 ValGlyAlaIleAlaIleProLeuTyrrIleProSerSerLeuThr---TyrrPheThrSer 81
Db 574 GTGGGTGCTTCTGTCATCCCATGTACGTACCTATGCTGACCGCGCTTGGACCTTC 633
QY 82 GlyLysGlnAlaCysValPheThrLeuIleThrAapTyrrLeuLeuCysThrAlaSerVal 101
Db 634 GCGCGGGGCTCTGCAAGCTGTGGCTGGGTGGTAGACTACTACTGTGTGCTCTCGGTGC 693
QY 102 TyrAenIleValLeuIleSerTyrrAapArgTyrrGlnSerValSerAenAlaValTyrr 121
Db 694 TTCACATGCTACTCATAGCTATGACCGATTCTCTGCTGACTGACTGAGCTGTCTCTAC 753
QY 122 ArgAlaGlnHisSerGlyThrTrpIleAlaIleThrGlnMetValAlaValTrpIlePhe 141
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QY 142 SerPheMetThrAsnGlyProMetIleLeuIleSerAapSerTyrrGln-----157
Db 814 GCTTCTCTGCTATGGGCTGCCATCTCTG-----AGTTGGGAGTACCTGTGTGTGT 864
QY 158 ---AenSerThrThrGlu-----CysGluProGlyPheLeuLysIleTyrrPheAla 174
Db 865 GCGAGTTTCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTTACACTGGTACTTCTC 924
QY 175 LeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaTyrrPheSerAla 194
Db 925 ATCAGCGGCTCCACCTCGAGTCTTTCAGCGCTTCTCCTCAGCGTTACCTTCTTCAACCTC 984
QY 195 HisIleTyrrTrpSerLeuTrpLysArgGluLysLeu-----SerArgCysLeuSer 211
Db 985 AGCATCTACCTGAACATCAGAGGGGCGACCCCGCTTGGCTTGTATGGGGCGCGTGAGGT 1044
QY 212 HisProValLeuProSerAapSerSerSer-----222
Db 1045 GCGCCAGAACCCCAACAGATCCCAAGCTCGCCCTCGCCACTTCCAGCTTCCCGCCAGCTGG 1104
QY 223 -----AspHisGlyHisSerCysArgGlnAapProAapSerArg-----235
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QY 313 AlaIleCysTrpAlaProTyrrSerLeuThrThrValIleTyrrSerPheProGluArg 332
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QY 373 LeuProValArgArgGlnSerThrProProHis 383
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RESULT 3
US-11-136-527-127
; Sequence 127, Application US/111136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI01086)
; CURRENT APPLICATION NUMBER: US/11/1136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Alignment Scores:
Pred. No.: 7,28e-46 Length: 2824
Score: 620.50 Matches: 153
Percent Similarity: 49.9% Conservative: 62
Best Local Similarity: 35.5% Mismatches: 147
Query Match: 30.5% Indels: 69
DB: 14 Gaps: 13

US-10-626-398-10 (1-389) x US-11-136-527-127 (1-2824)
QY 3 AlaAenAenSerThrIleAlaLeuThrSerIleLysLeuThrPheLeuMetSer 22
Db 413 GCGCGGGCTTCTCGCTCGCTGGACCGGTGC-----CTGGCTCGCTCATGGCG 463
QY 23 LeuLeuAlaIleAlaIleMetLeuGlyAenValValIleLeuLeuAlaPheLeuValAap 42
Db 464 CTGCTCATGTCGCGCCACAGTACTGGGCAACGGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
QY 43 ArgAenLeuArgHisArgSerAenTyrrPhePheLeuAenLeuAlaIleAlaAapPhePhe 62
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Db 644 GCGCGGGGCTCTGCAAGCTGTGGCTGGGTGGTAGACTACTACTGTGTGCTGCTGCTGCTGCT 703
QY 102 TyrAenIleValLeuIleSerTyrrAapArgTyrrGlnSerValSerAenAlaValTyrr 121
Db 704 TTCACATGCTACTCATGAGCTATGACCGATTCCTGTGCTGCTGCTGCTGCTGCTGCTGCT 763
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QY 370 uLysIleLeuProVal-----ArgAr 377
Db 1796 GATGCTCTCTTGTGTCCAGTGTGACAAAGAGGAGCGCAACAGCAGTAGTACCAGCAGAG 1855
QY 377 gGlnSerThrProHisAsnArg 385
Db 1856 ACAGTCGGTCATTTTTCACAGCGA 1880

RESULT 6
US-11-136-527-2030
; Sequence 2030, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2030
; LENGTH: 4095
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2030

Alignment Scores:
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Score: 407.50 Matches: 130
Percent Similarity: 40.5% Conservative: 84
Best Local Similarity: 24.6% Mismatches: 146
Query Match: 20.0% Indels: 169
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QY 74 rSerLeu---ThrTyrThrSerGlyLysGlnAlaCysValPheTyrPheLeuThrAs 93
Db 929 ATCATATGAACCGT-TGGGCACTGGGNACTTAGCTGGACCTTGGCTTCCATTGA 987
QY 93 pTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspTyrGln 113
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QY 113 nSerValSerAsnAlaValTyrTyrArgAlaGlnHisSerGlyThrTyrPheIleAlaTh 133
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QY 133 rGlnMetValAlaValTyrPheSerPheMetThrAsnGlyProMetIleLeuIleSe 153
Db 1105 GATGATTGCTGGCTTGGTTCATCTCTTCTATGGGCTCTGCCATCTTGTCTG 1164
QY 153 rAspSerTyrGlnAsnSerThr-----GluCysGluProGlyPheLeu 169
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QY 169 sLysTyrPyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189

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Db 1225 TGAGCCCAACCATCACCTTGGCAGCGGATCGCTGCTTTTACATGCTGTGCACCATCAT 1284
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Db 1285 GACTATT-----TTATACCTGGAGATCTATAAGGAAACTGAGAAGCGTACCAA 1332
QY 208 gCysLeuSer-----HisPr 213
Db 1333 AGAGCTGGCTGGCTACAGGCTCTGGCAGAGAAGCGGAGGACAGAAAACCTTGTTCACCC 1392
QY 213 oValLeuProSerAspSerSerSer----- 222
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QY 222 ----- 222
Db 1453 ATCCAGGAGGAAGTACGGTCTGCTGCTTCTGTTTCCACCACAGAGCTGGAAGCCAG 1512
QY 223 -----AspHisGlyHisSerCysArg-----GlnAspProAspSerAr 235
Db 1513 TGCCGAGCAGATGGACCAAGACCAACAGCAGCAGCAGCAGTTGGAAACAACAACAGATGCTGC 1572
QY 235 gAlaThrLeuProAlaArgLysGluThrThrAlaSer-----LeuGlySe 250
Db 1573 TGCCTCCCTG-----GAAACTCTGCTTCTCCGATGAAGAGGACATTTGGCTC 1620
QY 250 rAsp-----LysSerArgArgLysSerSerSerLeuLeuPr 261
Db 1621 AGAGACCAAGGCCCATCTATTCTTCTCAAGCTTCCAGGCCATAGCTCCATCTCAA 1680
QY 261 oSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLys----- 275
Db 1681 CTCTACCAAGTACCTCTCAGATACCTCGAGTGTCTCAACAGGACCTGGGGACTGT 1740
QY 275 ----- 275
Db 1741 GGATGTGGAGAGAAATGCTCACAAAGCTTTCAGGCCCAAGAGATGGGTGATGTGACAA 1800
QY 276 -----MetGlyPh 278
Db 1801 CTGTGAGAAGGATTTTACCAAGCTTCCCATCCAGTTAGAGTCTGCTGTGGACACAGGCAA 1860
QY 278 eLeuSerHisSerAspSerLeuAla----- 286
Db 1861 GACCTCTACCAACCACTCTCGGAGACAAGACCAAGCTACTTACTCTGTCTCTTCAA 1920
QY 287 -----LeuGlnGlnArgG1 291
Db 1921 GGAGCCCAAGCTGGCTAAGAGTTTGTCTCTCAAGACCAAGTACAGTACCAAGCGGAA 1980
QY 291 uHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerSerLeuAlaIleLeuLeuAla 311
Db 1981 GAGGATGTGCTCATCAAGGAGAGAGAGCGCCAGACGCTCAGTCGATCTTCTGCTAGC 2040
QY 311 aPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProG1 331
Db 2041 CTTTCATCATCAGTGGACCCCTACACATCATGGTCTGTGGTGAACACCTTCYGTGAC--- 2098
QY 331 uArgAsnLeuThrLysSerThrTyrTyrHisThrAlaPheTyrLeuGlnTyrPheAsnSe 351
Db 2099 ---AGTGCATACCCCAAAACCTATTGGAATCTGGGCTACTTGGCTGTGTATATCAACAG 2154
QY 351 rPheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeu 371
Db 2155 CACCGTGAACCTGTGTGTCTATGCCCTGTGCAACAAAACATTCAGAACCACTTCAAGAY 2214
QY 371 sIleLeuProVal-----ArgArgG1 378
Db 2215 GCTCTCTTGTGCCAGTGTGACAAAGAGGCGGCAACAGCAGTACCAGCAGAGACA 2274
QY 378 nSerThrProHisAsnArg 385

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Db 2275 GTCGGTCAATTTTTCACAGCGA 2296

RESULT 7

US-11-036-196-1495

Sequence 1495, Application US/11036196

Publication No. US20060078900A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Higgs, Brandon

APPLICANT: Castle, Arthur

APPLICANT: Blaschhoff, Michael

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5089-US

CURRENT APPLICATION NUMBER: US/11/036,196

PRIOR FILING DATE: 2005-01-18

PRIOR APPLICATION NUMBER: US/10/152,319

PRIOR FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US 60/292,335

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/297,523

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,810

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,807

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/315,047

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 60/324,928

PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867

PRIOR FILING DATE: 2001-11-01

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2221

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1495

LENGTH: 3578

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURES:

OTHER INFORMATION: Genbank Accession No. NM\_012527

US-11-036-196-1495

Alignment Scores:

Pred. No.:	4,356-26	Length:	3578
Score:	404.50	Matches:	130
Percent Similarity:	40.5%	Conservative:	84
Best Local Similarity:	24.6%	Mismatches:	146
Query Match:	19.9%	Indels:	169
DB:	11	Gaps:	15

US-10-626-398-10 (1-389) x US-11-036-196-1495 (1-3578)

QY 15 IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaMetLeuGlyAsnValVal 34

Db 242 GTCCTCATGGCTTTTAACTGGCTTCCTGGATTTGGTGGACCATCATTTGGCAACATCTT 301

QY 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54

Db 302 GTCATTGTGGCTTCAAGGTCAACAAACAGCTGAAGACAGTCAACACTACTTCTCTTA 361

QY 55 AsnLeuAlaIleAlaAspPheValGlyAlaIleAlaIleProLeuTyr-IleProSe 74

Db 362 AGCTGGGCTGTGCAGCTGATCATCGGGGTCAATTCATGAACCTGTTCACTACCTAC 421

QY 74 rSerLeu---ThrTyrTrpThrSerGlyGlnAlaCysValPheTrpLeuIleThrAs 93

Db 422 ATCATATGAACCGT-TGGGCACTGGGGAACCTTAGCCCTGGGACCTCTGGCTCTCCATTGA 480

QY 93 pTyrIleLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGl 113

Db 481 CTATGTGGCCAGCAATGCTCTGTATGAATCTGTGGTCATCAGCTTTTGACAGGTACTT 540

QY 113 nSerValSerAsnAlaValTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaTh 133

Db 541 TTCCATCACTAGGCCACTCACCTACGAGCCAAAGAACAA--ACAAAACGAGCTGGTGT 597

QY 133 rGlnMetValAlaValTrpIlePheSerPheMetThrAsnGlyProMetIleLeuIleSe 153

Db 598 GATGATTGGTCTGGCTTGGGTCTCTCTTGTCTATGGGCTCTCCATCTTGTCTG 657

QY 153 rAspSerTrpGlnAsnSerThrThr-----GluCysGluProGlyPheLeuIly 169

Db 658 GCATATCTTTGTAGGGAAGAGAACTGTGCCCCAGAGAAATGTTTCATTCAGTTTCTGAG 717

QY 169 sLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189

Db 718 TGAGCCCACTACCTACCTTCGGCAGCGGATCGCTGCTTTTACATGCTGTCACCATCAT 777

QY 189 lAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLysArg---GluLysLeuSerAr 208

Db 778 GACTATT-----TTATACTGGAGGATCTATAAGGAACTGAGAGAGCTACCAA 825

QY 208 gCysLeuSer-----HisPr 213

Db 826 AGAGCTGGCTGGCTTACAGGCTCTGGGACAGAGCGGAGGAGGAGAAACTTTTGTCCACC 885

QY 213 oValLeuProSerAspSerSerSer----- 222

Db 886 CACAGCGAGTTCTCGAAGCTGTAGCAGCTATGNACTGCACAGCAGGGGTGAAGAGTGC 945

QY 222 ----- 222

Db 946 ATCCAGGAGGAAGTAGCTGCTGCTCACTTCTGTTTCCACCACCAAGAGCTGCAAGCCAG 1005

QY 223 -----AspHisGlyHisSerCysArg-----GlnAspProAspSerAr 235

Db 1006 TGCCGAGCAGATGGACCAAGACCACAGCAGCAGCAGCAGCTTGGAAACAACAACAGTGTGC 1065

QY 235 gAlaThrProAlaArgLysGluThrAlaSer-----LeuGlySe 250

Db 1066 TGCTCTCCCTG-----GAAACTGTCTTCTCCGATGAAGAGGAGCATGGCTC 1113

QY 250 rAsp-----LysSerArgArgLysSerSerLeuLeuPr 261

Db 1114 AGAGACCAAGGCGCATCTATTCTTCTTCAAGCTTCCAGGCCATAGCTTCCATCTCAA 1173

QY 261 oSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLys----- 275

Db 1174 CTCTACCAAGCTACCGTCTCAGATAAAGCTGCAAGGTGTCCAACGAGGACCTGGGACTGT 1233

QY 275 ----- 275

Db 1234 GGATGTGGAGAGAAATGCTCAAGCTTCAAGGCCAGAGAGCATGGGTGATGGTGACAA 1293

QY 276 -----MetGlyPh 278

Db 1294 CTGTGAGAAGGATTTTCCCAAGCTTCCCATCCAGTTAGAGTCTGCGGTGGACAGGCAA 1353

QY 278 eLeuSerHisSerAspSerLeuAla----- 286

Db 1354 GACCTCTGACACCAACTCTCGGCAGACAGACACCGGCTACTTACCTCTGCTCTCAA 1413

QY 287 -----LeuGlnArgGl 291

Db 1414 GGAGGCCAGCTGGCTTAAGAGTTTGTCTCAAGACCAAGAAAGTCAAGTCAAGCGGAA 1473

QY 291 uHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAla 311

Db 1474 GAGGATGTGCTCATCAAGGAGAGAGAGGCGGCCAGAGCGTCAAGTGCATCTTCTAGC 1533



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QY 311 aPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPheProG1 331
Db 1534 CTTTCATCATCAGTGGACCCCTACACATCATGTCTCTGGTGAACACTTCTGTGAC-- 1591
QY 331 uArgAsnLeuThrLysSerTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSe 351
Db 1592 ----AGCTGCATACCCAAACCTATTGGAATCGGCTACTGGCTGTGTATATCAACAG 1647
QY 351 rPheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLy 371
Db 1648 CACCGTGAACCCGTGTGTCTATGCTGTGCAACAAACATTCAGAACCCCTTCAAGAC 1707
QY 371 sIleLeuProVal-----ArgArgG1 378
Db 1708 GCTCTCTTGTGTCAGTGTGCAAAAGGAAGAGCGCAACAGCAGTACCAGCAGAGACA 1767
QY 378 nSerThrProProHisAsnArg 385
Db 1768 GTCGGTCATTTTTCACACCGA 1789
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## RESULT 8

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US-11-127-877-17
; Sequence 17, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittlaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: Anyloid-Beta Protein Production
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/503,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-17
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Alignment Scores:
Pred. No.: 2,17e-26 Length: 1773
Score: 403.50 Matches: 129
Percent Similarity: 39.2% Conservative: 79
Best Local Similarity: 24.3% Mismatches: 152
Query Match: 19.8% Indels: 171
DB: 14 Gaps: 14
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US-10-626-398-10 (1-389) x US-11-127-877-17 (1-1773)

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QY 15 IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaIleMetLeuGlyAsnValVal 34
Db 205 GTCTTCATCGCTTCTTAACGGGCATCTCTGGCTTGGTACCATCATCGGCAACATCTCTG 264
QY 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54
Db 265 GTAATGTGTCTAATTAAGTCAACAGCAGCTGAAGACCGTCAACAACTACTTCTCTTA 324
QY 55 AsnLeuAlaIleAlaAspPheValGlyValIleAlaIleProLeuTyrIleProSer 74
Db 325 AGCTGGCCCTGTGCCGATCTGATATCGGGTCAITTCATGAATCTGTT----- 375
QY 75 SerLeuThrTyr-----TrpThrSerGlyLysGlnAlaCysValPheTrp 89
Db 376 ---ACGACCTACATCATCATGAATCATGCGCTTAGGGAACTTGGCCCTGTGACCTCTGG 432
QY 90 LeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyr 109
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Db 433 CTTCGCAATGACTAGTACCGCAGCAATGCTCTGTATGAATCTTCTGTCATCAGCTTT 492
QY 110 AspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAlaGlnHisSerGlyThrTrp 129
Db 493 GACAGATACTTTTTCATCAGCAGGCGCTCAGTACCGAGCAACAG-----ACAACA 546
QY 130 LysIleAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro 148
Db 547 AAGAGAGCCGCTGTGATGATCGCTGGCTGGGTGTCATCTCTTTGCTCTTTGGCTCT 606
QY 149 MetIleLeuIleSerAspSerTrpGlnAsnSerThrThr-----GluCysGlu 164
Db 607 GCCATCTTGTCTGCAATACTTTGTTGGAAGAGNACTGTGCTCTCCGGAGAGTGTCTC 666
QY 165 ProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIle 184
Db 667 ATTGAGTTCTCTCAGTGAGCCACCATTACTTTTGGCACAGCATCGCTGCTTTTATATG 726
QY 185 ProfileLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLys----- 202
Db 727 CTTGTCCACCATTTATGACTATT-----TTATCTGGAGCATCTATAAGGAACACT 774
QY 202 ----- 202
Db 775 GAAAAGCGTACCAAGAGCTTGTGCTGGCTGCAAGCTCTCGGACAGAGGAGCAGACAGAA 834
QY 202 ----- 202
Db 835 AACTTTGTCCACCCACCGGCGAGTTCTCGAAGTGCACAGTTCACGAACTTCAACAGCAA 894
QY 203 -----ArgGluLysLeuSerArgCys----- 209
Db 895 AGCATGAACCGCTCCACAGAGGAGTATGGCCGCTGCCACTTCTGGTTCAACACCAAG 954
QY 210 -----LeuSerHisProValLeuProSerAspSerSerSerSerSerAspHis-GlyHi 226
Db 955 AGCTGGAAACCCAGCTCCGAGCAGATGACCAAGACACACAGCAGCAGTGCACAGTTGGAAC 1014
QY 226 sSerCys-----ArgGlnAspProAspSerArgAlaThrLeu--- 238
Db 1015 AACATGATGCTGTGCTCCCTCGGAGAACTCCGCTCTCCGACGAGGAGGAGCATTTGCG 1074
QY 239 -ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSe 258
Db 1075 TCCGAGACGAGAGCCATCTACTCCATCGTGTCTCAAGCTTCCGGGTCAAGACCATCTCTC 1134
QY 258 rLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPh 278
Db 1135 AACTCCACCAAGTTACCC-TCATCGGACACCTCGAGGTGCTCGAGGAGAGTGGGAT 1193
QY 278 eLeuSer-----HisSerAspSerIleuAlaLeuGln----- 288
Db 1194 CGTGGACTTGGAGAGGAAAGCCGACAAGCTGCGAGGCCAGAGAGCGTGGAGTGAGG 1253
QY 288 ----- 288
Db 1254 CAGTTTTCCAAAAGCTTCTCCAGCTTCCCATCCAGTAGAGTCAGCCGTGACACAGC 1313
QY 288 ----- 288
Db 1314 TAAGACTTTCAGCTCAACTCCTCAGTGGGTAAAGAGCAGCGCCACTTACCTCTGTCTT 1373
QY 289 -----GlnAr 290
Db 1374 CAAGGAAGCCACTCTGGCCAGAGGTTTGTCTCTGAAGACCAGAGTTCAGATCACTAAGCG 1433
QY 290 gGluHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAl 310
Db 1434 GAAAGAGATGTCCTGGTCAGGAGAGAAAGCGGCCAGACCTCAGTCAGTCGATCTTGTCT 1493
QY 310 aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePhe 330
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Db 1494 TGCCTTCATCATCACTTGGACCCCATACAAACATCATGTTCTGTTGTAACACCTTTTGTGA 1553  
 Qy 330 oGluArgAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAs 350  
 Db 1554 C-----AGCTGCATACCCAAACCTTTTGGATCTGGGCTATCGCTGTGCTACATCAA 1607  
 Qy 350 nSerPheValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLe 370  
 Db 1608 CAGCACCCTGMAACCCCGTGTCTATGCTCTGTGCAACAAACATTCAGAACCACTTCAA 1667  
 Qy 370 uLysLeuProVal-----ArgAr 377  
 Db 1668 GATGCTGCTGCTGCGAGTGTGACAAAAAAGAGGGCGCAAGCAGCAGTACAGCAGAG 1727  
 Qy 377 gGlnSerThrProProHisAsnArgSer 386  
 Db 1728 ACAGTCGGTCATTTTTCACAAAGCGCGCA 1755

## RESULT 9

US-11-124-368A-14  
 ; Sequence 14, Application US/11124368A  
 ; Publication No. US20050287559A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michele Cargill  
 ; APPLICANT: James J. Devlin  
 ; APPLICANT: May Luke  
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
 ; FILE REFERENCE: CL001524  
 ; CURRENT APPLICATION NUMBER: US/11/124,368A  
 ; PRIOR FILING DATE: 2005-05-09  
 ; PRIOR APPLICATION NUMBER: US 60/568,845  
 ; PRIOR FILING DATE: 2004-05-07  
 ; PRIOR APPLICATION NUMBER: US 60/625,936  
 ; PRIOR FILING DATE: 2004-11-09  
 ; NUMBER OF SEQ ID NOS: 21112  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 1974  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-11-124-368A-14

## Alignment Scores:

Pred. No.: 2,5e-26 Length: 1974  
 Score: 403.50 Matches: 129  
 Percent Similarity: 39.2% Conservative: 79  
 Best Local Similarity: 24.3% Mismatches: 152  
 Query Match: 19.8% Indels: 171  
 DB: 14 Gaps: 14

US-10-626-398-10 (1-389) x US-11-124-368A-14 (1-1974)

Qy 15 lIeSerLeuThrPheLeuMetSerLeuLeuAlaAlaIleMetLeuGlyAsnValVal 34  
 Db 205 GTCTTCATCGCTTTCTTAACGGGCACTCTGGGCTTGGGACCATCATCGGCAACATCTGTG 264  
 Qy 35 ValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeu 54  
 Db 265 GTAATGTGTCATTTAAGTGTCAACAGCAGCTGAAGACGGTCAACACTACTTCTCTTA 324  
 Qy 55 AsnLeuAlaIleAlaAspPhePheValGlyAlaIleAlaIleProLeuTyrIleProSer 74  
 Db 325 AGCCTGGCCGTGCGCATCTGATTATTCGGGGTCATTTCAATGAATCTGTT----- 375  
 Qy 75 SerLeuThrTyr-----TrpThrSerGlyGlnAlaCysValPheTrp 89  
 Db 376 ---ACGACCTACATCATCATGAATCGATGGGCTTAGGGAACCTTGGCCTGTGACCTCTGG 432  
 Qy 90 LeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyr 109  
 Db 433 CTTCGCAATGACTAGTACCGCAGCAATGCCTCTGTATGAAATCTTCTGTGTCATCAGCTTT 492

Qy 110 AspArgTyrGlnSerValSerAsnAlaValTrpTyrArgAlaGlnHisSerGlyThrTrp 129  
 Db 493 GACAGATATCTTTTCCATCACGAGCGCTCACGATCCGAGCCAAACGA-----ACAACA 546  
 Qy 130 LysIleAlaThrGlnMetValAlaVal---TrpIlePheSerPheMetThrAsnGlyPro 148  
 Db 547 AAGAGAGCCGGGTGATGATCGTCTGGCTTGGTCTCTCTTGTCTCTTTGGGCTCCT 606  
 Qy 149 MetIleLeuIleSerAspSerTrpGlnAsnSerThrThr-----GluCysGlu 164  
 Db 607 GCCATCTTCTTGGCAATACTTGTGTGAAAGAGAACTGTGCTCCCGGAGAGTGTCTTC 666  
 Qy 165 ProGlyPheLeuLysLysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIle 184  
 Db 667 ATTCAGTTCCTCAGTGAGCCCACTTACTTTTGGCAGCAGCATCGCTCTTTATATG 726  
 Qy 185 ProfileLeuLeuValAlaTyrPheSerAlaHisIleTyrTrpSerLeuTrpLys----- 202  
 Db 727 CCTGTCAACCATATGACTATT-----TTATACTGGAGGATCTATAAGGAACT 774  
 Qy 202 ----- 202  
 Db 775 GAAAGCGTACCAAGAGCTTCTGCTGCTCTGCAAGCTCTGGCAGCAGAGGAGAGACAGAA 834  
 Qy 202 ----- 202  
 Db 835 AACTTTGTCCACCCACGCGCAGTTCGAAAGCTGCGAGTTCGAACTTCAACAGCAA 894  
 Qy 203 -----ArgGluLysLeuSerArgCys----- 209  
 Db 895 AGCATGAACCGCTCCAAACAGGAGGAGTATGCGCGCTGCCACTTCTGGTTCACACCAAG 954  
 Qy 210 -----LeuSerHisProValLeuProSerAspSerSerSerSerSerSerSerHis-GlyHi 226  
 Db 955 AGCTGGAACCCAGCTCCGAGCAGATGGACCAAGACCAACAGCAGCAGTGTGGAAC 1014  
 Qy 226 sSerCys-----ArgGlnAspProAspSerArgAlaThrLeu-- 238  
 Db 1015 AACAAATGATGTGCTGCTGCTCCCTGGAGAACTCCGCTCTCCGAGGAGGAGGAGGAGTGC 1074  
 Qy 239 -ProAlaArgLysGluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSe 258  
 Db 1075 TCCGAGACGAGAGCCATCTACTCCATCTGTCTCAAGCTTCCGGGTACAGCAGCAGCAGCCTC 1134  
 Qy 258 rLeuLeuProSerIleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPh 278  
 Db 1135 AACTCCACCAAGTTACCC-TCATCGGACAACTCGCAGGTGCTCGAGGAGGAGCTGGGAT 1193  
 Qy 278 eLeuSer-----HisSerAspSerLeuAlaLeuGln----- 288  
 Db 1194 GGTGGACTTGGAGAGGAAAGCCGACAGCTGCGAGGCCAGAGAGCGTGGACGATGGAGG 1253  
 Qy 288 ----- 288  
 Db 1254 CAGTTTTCCAAAAGCTTCTCCAGCTTCCCATCCAGCTAGAGTACGCGGTGACACAGC 1313  
 Qy 288 ----- 288  
 Db 1314 TAAGACTTCTGACGTCAACTCTCTAGTGGTAAGAGCAGCGCCACTCTACCTCTGTCTT 1373  
 Qy 289 -----GlnAr 290  
 Db 1374 CAAGAGACCCACTCTGGCCAAAGAGTGTGCTCTGAAGACCAAGAGTCAGATCATCAAGCG 1433  
 Qy 290 gGluHisIleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuAla 310  
 Db 1434 GAAAGAGATGTCCTTGGTCAAGAGAAAGAGGCGGCCAGCCCTCAGTGGCATCTTGTCT 1493  
 Qy 310 aAlaPheAlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePhePr 330  
 Db 1494 TGCCTTCATCATCTTGTGACCCCAACATCATCATGTCTGTGTGGAACACCTTTGTGA 1553  
 Qy 330 oGluArgAsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAs 350

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Db 1554 C-----AGTCGATACCAAAACCTTTTGGATCTGGGCTACTGGCTGTGTCTACATCAA 1607
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Qy 350 nSerPheValaAnProPheLeuTyProLeuCysHisLysArgPheGlnLysAlaPheLe 370
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1608 CAGCACCGTGAACCCCGGTGCTATGCTCTGTGCAACAAACATTCAGAACCCACTTTCAA 1667
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 370 uLysLeuProVal-----ArgAr 377
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1668 GATGCTGCTGTGTGCCAGTGTGACAAAAAAGAGCGCAAGCAGCAGTACCAGCAGAG 1727
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 377 gGlnSerThrProHisAsnArgSer 386
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1728 ACAGTCGGTCAATTTTTCACAGCGCGCA 1755
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RESULT 10
US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2435
; TYPE: DNA
; LENGTH: 2733
; ORGANISM: Rattus norvegicus
US-11-136-527-2435

Alignment Scores:
Pred. No.: 4,68e-26 Length: 2733
Score: 402.50 Matches: 125
Percent Similarity: 39.4% Conservative: 81
Best Local Similarity: 23.9% Mismatches: 150
Query Match: 19.8% Indels: 167
DB: 14 Gaps: 17

US-10-626-398-10 (1-389) x US-11-136-527-2435 (1-2733)

Qy 4 AsnAsnSerThrIleAlaLeuThrSerIleLys----- 14
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 992 AATGAAGGACCTGTCAACGGCACCCGGTAATCACCAGGCTTTGGAAAGCCATGGACTG 1051
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 15 -----IleSerLeuThrPheLeuMetSerLeuLeuAlaIleAlaIleMetLeuGly 31
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1052 TGGGAAGTCATTACTATTGCTGAGTTGTGACTGCGGTGTGCTGAGCTGATGACCATTTGCGC 1111
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 32 AsnValValIleLeuAlaPheIleValAspArgAsnLeuArgHisArgSerAsnTy 51
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Db 1112 AATGCTTGGTCTATGCTCTCTCAAGTCAACAGTCACGCTCAAGACAGTTAACCACTAC 1171
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Qy 52 PhePheLeuAsnLeuAlaIleAlaAspPheValGlyAlaIleAlaIleProLeuTy 71
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Db 1172 TACCTGCTCAGCTTGGCTGTGGAGACCTCATCATTTGGGATCTTCTCCATGAACCTTAC 1231
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Qy 72 IleProSerSerLeuThrTy-----TriThrSerGlyLysGlnAlaCys 86
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1232 -----ACGACCTACATCTCATGGGAGCGTGGTCTCTCGGAGTCTGGCTGT 1279
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Qy 87 ValPheTriPheLeuThrAspTyLeuLeuCysThsAlaSerValTyRsnIleValLeu 106
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1280 GACCTTTGGCTGCACTCGACATATGTAGCCAGCAATGCTTCTGTCAATGAACCTTCTGGTG 1339
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 107 IleSerTyAspArgTyGlnSerValSerAsnAlaValTriPtyrArgAlaGlnHisSer 126
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1340 ATTAGTTTGAUGCTTACTTTTCCATCACAGACCACTGACGTACCGGGCCAAAGCGT--- 1396
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy 127 GlyThrTriPlyAlaIleAlaThrGlnMetValAlaVal---TriPhePheSerPheMetThr 145
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1397 ---ACCCCAAAAGAGGGCTGGCATCATGATTGGCTTAGCATGGCTGGCTCTCTTTCATCCTC 1453
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 146 AsnGlyProMetIleLeuIleSerAspSerTriPdnAen----- 158
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1454 TGGGCGCCAGCCATCCTC-----TGCTGGCAGTACTTGGTGGGAAGCGGACAGTA 1504
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 159 SerThrThrGluCysGluProGlyPheLeuLysLysTriPtyrPheAlaLeuProThrSer 178
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1505 CCACCTGATGAGTGCAGATCCAGTTCTCTCAACCCACCATCATTCTTTGGGACTGCC 1564
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 179 LeuLeuGluPheLeuIleProIleLeuValAlaTyPheSerAlaHisIleTy--- 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1565 ATTGTCCTTCTACATCCCTGTCTCCGTGATGACCATCTCTACTGCGGATCTACCGG 1624
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 197 ----- 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1625 GAGACAGAGAAGCGAACCAAGGACTGCTGCTGACCTCCAAGGTTCTGATTCTGTGGCAGAA 1684
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 197 ----- 197
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1685 GCCAAGAAGAGAGAGCCAGCTCAAAGGACCCTGCTCAGATCTTCTTTAGTGCCTTAGA 1744
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 198 -----TriSerLeu----- 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1745 CCCAGCTGGGCCAGAGAGAAAGGAATCAGGCTCTCTGTCATCTCTCCGTAGAGCACC 1804
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 201 -----TriP---LysArgGlu 204
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1805 TCACAACAGAGAAAGACAAACCCAGGCCACTGACCTAAGTGTGCTGAGTGGGAAAAGGCTGAG 1864
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 205 LysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp--- 223
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1865 CAGGTTACTACTGTAGCAGCTACCCC-----TCTTCAGAGGATGAA 1906
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 224 -----HisGlyHisSerCysArgGlnAsp 231
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1907 GCCAAGCCCAACACTGACCCCTGCTTTCAATGGTCTACAAGAGTGAGGCCAAGGAAGC 1966
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 232 ProAspSerArgAlaThrLeuProAlaArgLysGluThr-----ThrAlaSerLeu 248
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1967 CCGGGGAAGGAATCCAATACCAAGAGACCAAGGAACAGTTGTGAACACCCGGACTGAA 2026
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 249 GlySerAspLysSerArgArgLysSerSerLeuLeuPro---SerIleArgAlaTyLys 267
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2027 AACAGTGACTATGACACTCCCAATATCTTTCTGTCTCCAGCTGTGCTCAGACACTCAAG 2086
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 268 AsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp----- 283
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2087 AGTCAGAAAGTGTGTGGCTTATAGTTCCGATTTGGTGGTAAAGCCGATGGGACCCAGGAG 2146
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 283 ----- 283
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2147 ACTTAAATGGTGTGCGAAAGTGAATCATGCCCTGTCTTCCAGTGTCCAAAGAC 2206
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 284 -----SerLeuAlaLeuGlnArgGluHisIle 293
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2207 CCTTCAACAAAAGGTCGCGATCCCAACCTCAGTCTCAATACCAACCAAGAGAGAAATG 2266
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 294 GluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPheAla 313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2267 GTTCTGGTCAAGAGAGGAACGGCTCAGACCTTGAGTGGCCATCTCTCTGCGCTTCATC 2326
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 314 IleCysTriPAlaProTySerLeuThrThrValIleTySerPhePheProGluArgAsn 333
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2327 ATCAGATGGACCCCTTATAACATC---ATGGTCTGGTGTTCACCTTCTGTGACAAGTGT 2383
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 334 LeuThrLysSerThrTriPtyrHisThrAlaPheThrLeuGlnTriPheAsnSerPheVal 353
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2384 GTCCCCGTCAACCTCTGG---CACTTGGGTACTGGCTGTGTCTATGTCAACAGCACCATC 2440
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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; Sequence 3114, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3114
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-3114

Alignment Scores:
Pred. No.: 4,02e-25 Length: 2633
Score: 392.00 Matches: 117
Percent Similarity: 44.2% Conservative: 71
Best Local Similarity: 27.5% Mismatches: 145
Query Match: 19.3% Indels: 93
DB: 14 Gaps: 13

US-10-626-398-10 (1-389) x US-11-136-527-3114 (1-2633)

Qy 23 LeuLeuAlaIleAlaIleMetLeuGlyAsnValValValIleLeuAlaPheIleValAsp 42
Db 246 CTCCTGCTCTTAGCTAGCTACGACGAGCAACTCTAGTGACTCACTCTTCAAGTCAAC 305
Qy 43 ArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAspPhePhe 62
Db 306 ACCGAGCTCAGACAGTCACACACTACTCTCTGCTGAGCCTGGCCTGACCTCATC 365
Qy 63 ValGlyAlaIleAlaIleProLeuTyrIleProSerSerLeuThr---TyrTrpThrSer 81
Db 366 ATTGGCACCTTCTCCATGAACCTCTATACCACTGCTACCTGCTCATGGGCCACTGGGCTCTG 425
Qy 82 GlyLysGlnAlaCyeValPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerVal 101
Db 426 GGCACACTGGCTGTGAACCTCTGGCTGGCCCTGGACTATGTGGCCAGCAACGCTCTGTC 485
Qy 102 TyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaValTrpTyr 121
Db 486 ATGAATCTTCTGCTCATCAGCTTTGACCGTTACTTCTCGGTGACCGACCCCTGAGCTAC 545
Qy 122 ArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAlaVal---TrpIle 140
Db 546 CGAGCCAAAGCGC-----ACTCCCGAAGGGCAGCTCTGATGATTGGCCTAGCATGGCTG 599
Qy 141 PheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGlnAsnSerThr 160
Db 600 GTTTCCTCTGTTCTCTGGGCCCCGAGCACTCTCTTC-----TGGCAATACCTAGTT 650
Qy 161 ThrGlu-----CysGluProGlyPheLeuLysIleSerTrpTyrPhe 173
Db 651 GGGGAGCGGACAGTCTGCTGGCAGTGTCTATCATCTCAGTTCTCTCTCCCAACCCATCATC 710
Qy 174 AlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuLeuValAlaIleThrPheSer 193
Db 711 ACTTTTGGCACAGCCATGGCCCGCCTTCTACTCTCCCTGTCCAGGTCAAG----- 758
Qy 194 AlaHisIleTyrTrpSerLeuTrpLys-ArgGluLysLeuSer----- 207
Db 759 TGTACACTGTACTGGCGCACTATACCGGGAGACAGAAACCGAGCCCGGAGTGGCGCGCC 818
Qy 208 ----ArgCysLeuSerHisProValLeuProSerAspSerSerSerAspHisGlyHis 226
Db 819 CTGACAGGCTCTGAGACACAGGCAAGGTGGTGGCAGCAGCAGCAGCAGTCTCAGAGAGGTCA 878

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Qy	226	sSerCyArGlnAAspProAAspSerArgAlaThrLeuProAlaArgLysgluThrThrAl	246
Db	879	CAGC-----CAGGGGTGAAGGCTCAACCGAGTCGCTCCAGCGCGCGCTGC	923
Qy	246	a-----SerLeuGlySerAspLysSerAr	254
		:::	:::
Db	924	TGCGGCTGTTGCGGGCACCCAGGCTCTCCAGGCTTACAGCTGGAAGGAAGAAGAG	983
Qy	254	gaTg-----LysSerSerLeuLeuProSerIleArgAlaTyrIlysAenSe	269
Db	984	GAGGATCAAGGCTCCATGGAGTCCCTCACATCTCCGAAGGTGAGGAGCTGCTCAGAA	1043
Qy	269	rAsnValIleAlaSerIysMetGlyPheLeuSerHisSerAspSerLeuAla	286
Db	1044	GTG-GTGATCAAGATGCCCATG-----GTAGATTCTGAAGCACACAGGCACC	1087
Qy	286	-----	-----
Db	1088	CACCAAGCAGCCTCCAAAAGCTCCCAAATACAGTCAAGAGGCCCAACCAAGAAAGCGC	1147
Qy	287	-----LeuGlnGlnArgGluHi	292
		:::	:::
Db	1148	AGACCGAGGGCGGCAAGGGCCAAAACCCCGAGGAGGAACAGCTGGCCCAAGAGAAAGAC	1207
Qy	292	sileGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaAlaPh	312
Db	1208	CTTCTCACTGGTCAAGGAGGAAGAGGAGCTCGGAGCCCTGAGTGCCATCTCTGGCGCTT	1267
Qy	312	eAlaIleCyETrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluAr	332
		:::	:::
Db	1368	CATCCTCACTGGAGCACCATATACATCATGTGTCTGGTATCTACCTTCTGC-----AA	1321
Qy	332	gAsnLeuThrIlysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAenSerPh	352
		:::	:::
Db	1322	GGACTGTGTCTCTGAACCCCTGTGGGAGTGGGGCTACTTGGCTATGTCTACGTCAACAGCAC	1381
Qy	352	eValAsnProPheLeuTyrProLeuCyHisLysArgPheGlnLysAlaPheLeuLysIl	372
Db	1382	TGTCAACCCCATGTGCTATGTACACTGTGCACAAAGACCTTCGGGGACACAGTTCCCGCTGCT	1441
Qy	372	eLeuProValArg	376
Db	1442	GCTGCTCTCGCGC	1454
RESULT 13			
US-11-136-527-751			
; Sequence 751, Application US/11136527			
; Publication No. US20050287570A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William M			
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes			
; FILE REFERENCE: 031896-041000 (AM101086)			
; CURRENT APPLICATION NUMBER: US/11/136,527			
; CURRENT FILING DATE: 2005-05-25			
; PRIOR APPLICATION NUMBER: US 60/574,294			
; PRIOR FILING DATE: 2005-05-26			
; NUMBER OF SEQ ID NOS: 362830			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 751			
; LENGTH: 3741			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
US-11-136-527-751			

Alignment Scores:		
Pred. No.:	1,188-24	Length:
Score:	389.00	Matches:
Percent Similarity:	41.1%	Conservative:
Best Local Similarity:	23.3%	Mismatches:
Query Match:	19.1%	Indels:
DB:	14	Gaps:
		14
		3741

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US-10-626-398-10 (1-389) x US-11-136-527-751 (1-3741)
QY      1 MetLeuAlaAsnSerThrIleAlaLeuThrSerIleIleSerLeuThrPheLeu 20
Db      1030 ATGTGTGAGGGGAACAGGACAGCATGGCCAGCCCTCAGCTGCTGCCCTGTGGTGGTGT 1089
QY      21 MetSerLeuAlaIleAlaIleMetLeuGlyAsnValValIleValIleLeuAlaPheIle 40
Db      1090 CTWAGTAGTATCTCCCTGCTCACAGTGGGCGCTCAACACTGCTGTGTGTAYGCGWTGCR 1149
QY      41 ValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAlaAsp 60
Db      1150 AGTGARCGAAGCTACACACCGTGGCAACCTRTACATTGTGAGCTGTGCTGCTGCGAGAC 1209
QY      61 PhePheValGlyAlaIleAlaIlePro-----LeuTyrIleProSerSerLeuThr 77
Db      1210 CTGATTGAGGGGAGTGTCAATGCCCATGACATCTCTATCTY-----ATCATGAGY 1263
QY      78 TyrTrpThrSerGlyLysGlnAlaCysValPheTrpLeuIleThrAspTyrLeuLeuCys 97
Db      1264 AAGTGGTCTCTGCGCGCCCTCTGCTCTTTTGGCTTCTATGATATATGTCGCCAGC 1323
QY      98 ThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 117
Db      1324 ACRGATCATCTTTAGTGTCTTCACTCTGTGTATGATGCTGCTACGCTCTGTCTCCAGCAA 1383
QY      118 AlaValTrpTyrArgAlaGlnHisSerGlyThrTrpLysIleAlaThrGlnMetValAla 137
Db      1384 CCCCTCCGTCAGTCTGAGGTAYCGAACCAGAACCGCGTTCMGCTACC-----ATCTGGGG 1440
QY      138 ValTrpIlePheSerPheMetThrAsnGlyProMetIleLeuIleSerAspSerTrpGln 157
Db      1441 GCCTGGTCTTCTCTCTGCTGGGTATACCTATCTT-----GGCTGGCAT 1488
QY      158 Asn-----SerThrThrGluCysGluProGlyPheLeuLys 169
Db      1489 CACTTCAYGCCCYRGCCCGCCAGAGCTTCGGGAAGAAVAGTGTGAGACAGATTTCTACAAT 1548
QY      170 LysTrpTyrPheAlaLeuProThrSerLeuLeuGluPheLeuIleProIleLeuVal 189
Db      1549 GTCACTTGGTTCAAGATCATGACGTCATATATATATATATATATATATATATATATATAT 1608
QY      190 AlaTyrPheSerAlaHisIleTyrTrpSerLeuTyrLysArgGluLysLeuSerArgCys 209
Db      1609 CTGTGCTTCTATGTGAAGATCTACAGGCTGTG-----CGCGACACTGTGACGACCGCCAG 1665
QY      210 LeuSerHisProValLeuProSerAspSerSer-----SerSerAspHisGly 225
Db      1666 CTCACCAACGGGTCCCTCCCTWCCTTTTAVAGAAATCAAGCTGAGCTCGASGATRCCAAR 1725
QY      226 HisSerCysArg-----Gln 230
Db      1726 GARGGTGCCAAGAAACCTCGGARAGAGTCTCCCTGGGGGGTTCWGAARAGGCGCRCAAGA 1785
QY      231 AspPro-----AspSerArgAlaThrLeuProAlaArgLysGluThrAla 246
Db      1786 GACCCCTASTGKAGWCTGATCAGAAGTCAACATCTGAAGACCCCAAGRTGACCTCTCCR 1845
QY      247 SerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIleArg----- 264
Db      1846 ACTGTCCTTCAGCAGAGGGGGAAGGGAACAGTACACAGYCCCTGTTTCGTCTCTGAC 1905
QY      265 -----AlaTyrLysAsnSerAsn 270
Db      1906 RTCATGCAGAMACAGYCTGTGCTGAGGAGATGYCAGGGGCTCAAGGCCAATGAYCAG 1965
QY      271 VallIleAlaSer-----LysMetGlyPhe 278
Db      1966 RCCTTGAGCCAGCCCAAAATGATGAGCAGAGCCTGARTCTTGTGCGCGGATCAGTGAG 2025
QY      279 LeuSerHisSerAspSerLeuAlaLeuGlnGln----- 289
Db      2026 ACATCAGAGGAYCAGACCTTGTGTGATCBACAGTCTCTCTCCCGACACACAGACTCAGAC 2085
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QY      289 -----ArgGluHis----- 289
Db      2086 ACMAGCATAGACCAGGGGCGGCGCARAGTCAAAKCAGAGAAGCGGGTCTTAACAGYGCCTG 2145
QY      290 ----- 292
Db      2146 GAYTACATCAAAARTCACCTGGAGAGGCTCCGCTCACAATCCAGACAGTATGTGTCCGGG 2205
QY      293 IleGluLeuPheArgAlaArgLysLeuAlaLysSerLeuAlaIleLeuLeuAlaPhe 312
Db      2206 YTGCACTTGAACCGGAGCGGAGGAGCAGCAAGCAGATTTGGGTTTATCATGTCGCGGTTTC 2265
QY      313 AlaIleCysTrpAlaProTyrSerLeuThrThrValIleTyrSerPhePheProGluArg 332
Db      2266 ATTCTCTGCTGATTCCTTATTCATCTTCTTCATGGTCATTTGCTCTTGC-----AAS 2319
QY      333 AsnLeuThrLysSerThrTrpTyrHisThrAlaPheTrpLeuGlnTrpPheAsnSerPhe 352
Db      2320 AGCTGCTGCAGYGAACCYRTGCAYATGTTCCACATTTGGCTGGGCTACATCACTCCAGC 2379
QY      353 ValAsnProPheLeuTyrProLeuCysHisLysArgPheGlnLysAlaPheLeuLysIle 372
Db      2380 CTGAACCCCTCATCTACCCCTGTGCAACGAGAACTTCAAGAGACATTTCAAAAAAATT 2439
QY      373 LeuProValArg 376
Db      2440 CTGCACATTCGT 2451

RESULT 14
US-11-136-527-2377
; Sequence 2377, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2377
; LENGTH: 1862
; TYPES: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2377

Alignment Scores:
Pred. No.: 7,33e-25 Length: 1862
Score: 387.00 Matches: 115
Percent Similarity: 44.4% Conservative: 63
Best Local Similarity: 28.7% Mismatches: 139
Query Match: 19.0% Indels: 84
DB: 14 Gaps: 16

US-10-626-398-10 (1-389) x US-11-136-527-2377 (1-1862)
QY      4 AsnAsnSerThrIleAlaLeuThrSerIleLysIleSerLeuThrPheLeuMetSerLeu 23
Db      69 TCCAACTGCACCCACCCACAGCTCCGCTGAACATTTCTAAGGCCATTTCTGCTTGGGGTG 128
QY      24 -----LeuAlaIleAlaIleMetLeuGlyAsnValValIleValIleAlaPhe 39
Db      129 ATCTTGGGGGCGCTCATCATTTTCGGAGTCTCGGGAACATTTAGTATCTCTCTCAGTG 188
QY      40 IleValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleAla 59
Db      189 GCCTGTCTATCGGCATCTGCACTCCGCTGACTCACTACTACTTGTGTCRCYTGCTGCGCA 248
QY      60 AspPhePheValGlyAlaIleAlaIleProLeu-----TyrIleProSerSerLeuThrTyr 78
```

Db	249	 GACCTCCTCCTCACCTCCACTGCTGCTGCCCTTCTCTGCCACTCTTTGAGATCTTGCGGCTAC	308
Qy	79	 TTPThrSerGlyLysGlnAlaCysValPheTTPLeuLeuThrAspTyrLeuLeuCysThr	98
Db	309	 TGGCCCTTTGGCAGGGTGTCTCAATATCTGGCGCGCGTGGACGCTTATGCTGCACA	368
Qy	99	 AlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAla	118
Db	369	 GCGTCCATCATGGCCCTCTGCATCATCTCCATGACCGATACATTGGTGTGAGTACCCG	428
Qy	119	 ValTTPTrpArgAlaGlnHisSerGlyThrTTPTrpLysIleAlaThrGln	134
Db	429	 CTGGCTATATCCACC-----ATTGTCCACCCAGAGGAGGGGCGTC	467
Qy	135	 -----MetValAlaValTTPIlePheSerPheMetThrAsn-----GlyProMetIleLeu	151
Db	468	 AGGCTCTGCTGCGTCTGGGTCTTCTTGGTCACTCTCCATCGACCCCTGTTCTC---	524
Qy	152	 IleSerAspSerTTPGlnAsnSerThrThrGlu-----Cys-----	163
Db	525	 -----GGCTGGAGGACCGCGCTCCAGAGGATGAGACCATCTGCCAGATCAATGAG	575
Qy	164	 GluProGlyPheLeuLysLysTTPTrpPheAlaLeuProThrSerLeuLeuGluPheLeu	183
Db	576	 GAGCGCGCTACGTG-----CTGTCTCAGCGCTGGGCTCTTCTCTAC	617
Qy	184	 IleProIleLeuLeuValAlaTyrPheSerAlaHisIleTyrTTPSerLeuTTPLysArg	203
Db	618	 GTGCCATCGGCATCAVCTCTGGTTATGTACTGTGAGTCTAC---GTAGTAGCCAGAGA	674
Qy	204	 GluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerAsp	223
Db	675	 GAA-----AGCGGGCGCTCAAGTCGGC-----CTCAAGACGGACAGTCAGACTCAGAG	725
Qy	224	 HisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLysGlu	243
Db	726	 -----CAAGTGACGCTCCGCATCCACCGTAA	752
Qy	244	 ThrThrAlaSerLeuGlySerAspLysSerArgLysSerSerLeuLeuProSerIle	263
Db	753	 AATGTCCCTGCAGAAAGCGCGGAGTCAGCAGTCCCAAGAATAAGACTACTCTCTCAGTG	812
Qy	264	 ArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSerAsp	283
Db	813	 AGGCTGCTCAAGTTTCT-----	830
Qy	284	 SerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAlaLys	303
Db	831	 -----CGAGAGAAGAAGCTGCCAAG	851
Qy	304	 SerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTTPAlaProTyrSerLeuThrThr	323
Db	852	 ACGCTGGGCATCGTGGTGGTGTCTGCTCTGCTGGCTGCCGTTCTCTCCTAGTGATG	911
Qy	324	 ValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTTPTrpHisThrAla	343
Db	912	 CCCATTTGGGTCTTCTCCCGATTTCAAG---CCTTCGGAAACCGTTTAAAAATAGTA	968
Qy	344	 PheTTPLeuGlnTTPPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisLys	363
Db	969	 TTTTGGCTCGGTATCTAAATAGTTGCACTCAACCTCATATACCATGTCTCCAGCCAG	1028
Qy	364	 ArgPheGlnLysAlaPheLeuLysIleLeuProVal-----ArgArgGlnSer	379
Db	1029	 GAGTTTCAAGAAAGCCTTTTCAAGATGTCTCGGAATCCAGTGTCTTCGCAAGAGGCAGTCT	1088
Qy	380	 Thr 380	
Db	1089	 TCC 1091	

RESULT 15  
US-11-127-877-14

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QY 183 LeuIleProIleLeuLeuValAlaIleTyrPheSerAlaHisIleTyrTrpSerLeuTrpLys 202
Db   ::::: ::::: ::::: ::::: ::::: :::::
1016 TACCTGCCTCTGCCATCATCTCTGGTCATGTACTGCCGCTCTAC---GTGGTGGCCAAG 1072
QY 203 ArgGluLysLeuSerArgCysLeuSerHisProValLeuProSerAspSerSerSerSer 222
Db   ::::: ::::: ::::: ::::: ::::: :::::
1073 AGGGAG-----AGCGGGGCTCAAGTCTGGC---CTCAAGACCGCAAGTCGGACTCG 1123
QY 223 AspHisGlyHisSerCysArgGlnAspProAspSerArgAlaThrLeuProAlaArgLys 242
Db   ::::: ::::: ::::: ::::: ::::: :::::
1124 GAG-----CAAGTGACGCTCCGCATCCATCGG 1150
QY 243 GluThrThrAlaSerLeuGlySerAspLysSerArgArgLysSerSerLeuLeuProSer 262
Db   ::::: ::::: ::::: ::::: ::::: :::::
1151 AAAAAGCGCCCGGACGAGGCGAGCGGATGGCCAGCGCCAAAGACGACACTTCTCA 1210
QY 263 IleArgAlaTyrLysAsnSerAsnValIleAlaSerLysMetGlyPheLeuSerHisSer 282
Db   ::::: ::::: ::::: ::::: ::::: :::::
1211 GTGAGGCTCTCAAGTCTCC----- 1231
QY 283 AspSerLeuAlaLeuGlnGlnArgGluHisIleGluLeuPheArgAlaArgLysLeuAla 302
Db   ::::: ::::: ::::: ::::: ::::: :::::
1232 -----CGGAGAGAAGAAAGCGGCC 1249
QY 303 LysSerLeuAlaIleLeuLeuAlaAlaPheAlaIleCysTrpAlaProTyrSerLeuThr 322
Db   ::::: ::::: ::::: ::::: ::::: :::::
1250 AAAACGCTGGGCATCGTGGTCGGCTCTTCGTCCTCTGCTGGCTGCTTTTCTTAGTC 1309
QY 323 ThrValIleTyrSerPhePheProGluArgAsnLeuThrLysSerThrTrpTyrHisThr 342
Db   ::::: ::::: ::::: ::::: ::::: :::::
1310 ATGCCCATTTGGTCTTTCTTCCTGATTTCAAG---CCCTCTGAACACGTTTTTAAATA 1366
QY 343 AlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHis 362
Db   ::::: ::::: ::::: ::::: ::::: :::::
1367 GTATTTTGGCTCGGATATCTAAACAGCTGCATCACCCCATCATATACCCATGCTCCAGC 1426
QY 363 LysArgPheGlnLysAlaPhe-----LeuLysIleLeuProValArgGlnSer 379
Db   ::::: ::::: ::::: ::::: ::::: :::::
1427 CAAGAGTTCAAAAGGCGCTTTCAGATGTCTTGAGAAATCCAGTGTCTCGCAGAAAGCAG 1486
QY 380 ThrProProHis 383
Db   :::::
1487 TCTTCAACAT 1498
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Job time : 589 secs



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